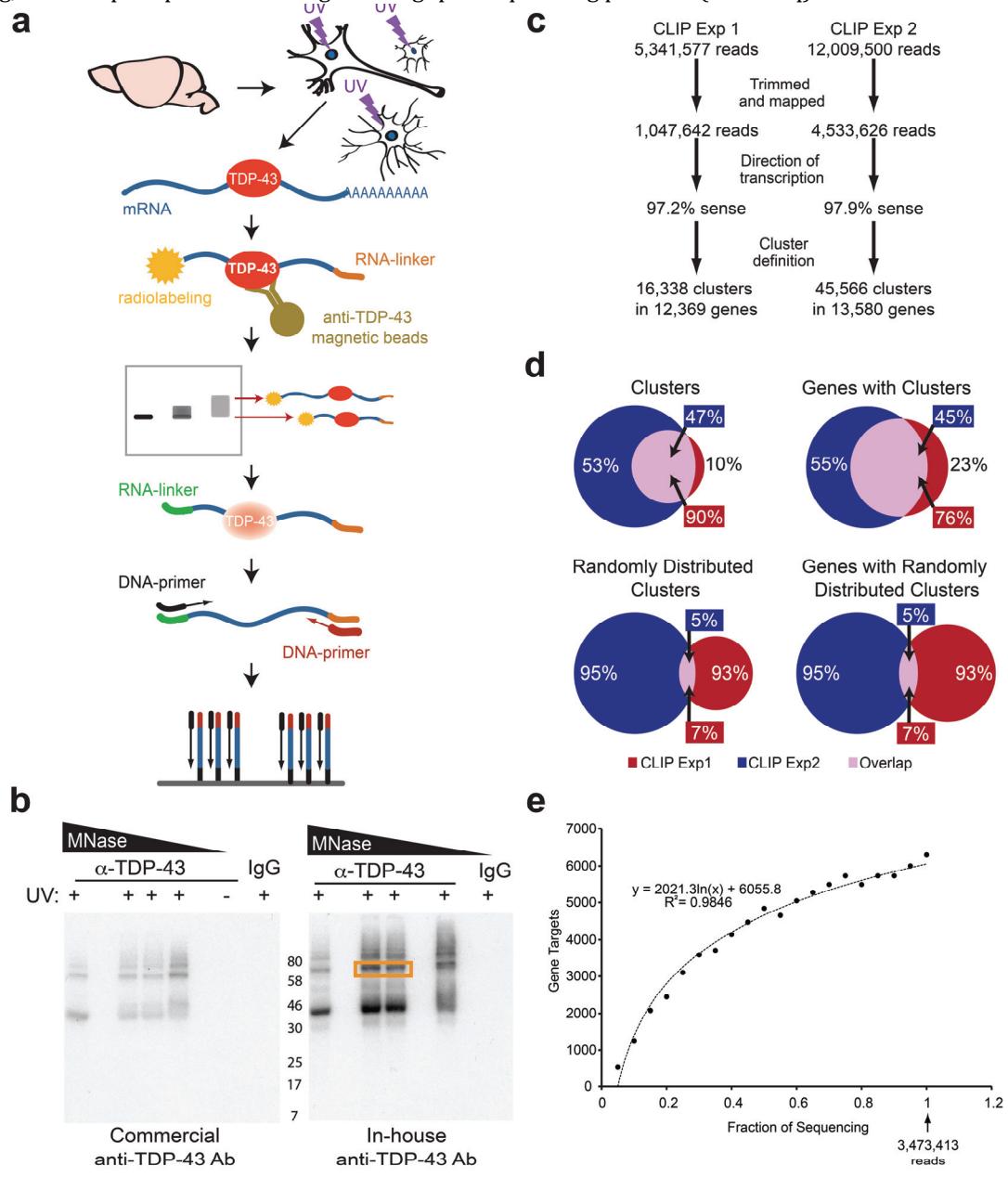


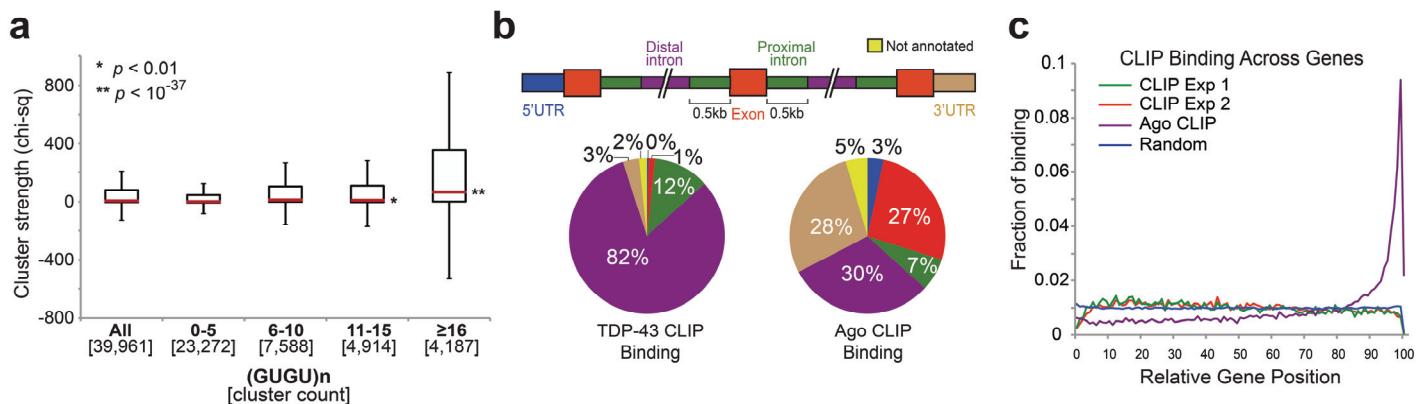
Long pre-mRNA depletion and RNA missplicing contribute to neuronal vulnerability from loss of TDP-43

Polymenidou M*, Lagier-Tourenne C*, Hutt KR*, Huelga SC, Moran J, Liang TY, Ling SC, Sun E, Wancewicz E, Mazur C, Kordasiewicz H, Sedaghat Y, Donohue JP, Shiue L, Bennett CF, Yeo GW and Cleveland DW

Supplementary Figure 1 TDP-43 CLIP-seq method, reproducibility and saturation of binding sites. (a) Schematic representation of cross-linking, immunoprecipitation and high-throughput sequencing protocol (CLIP-seq).

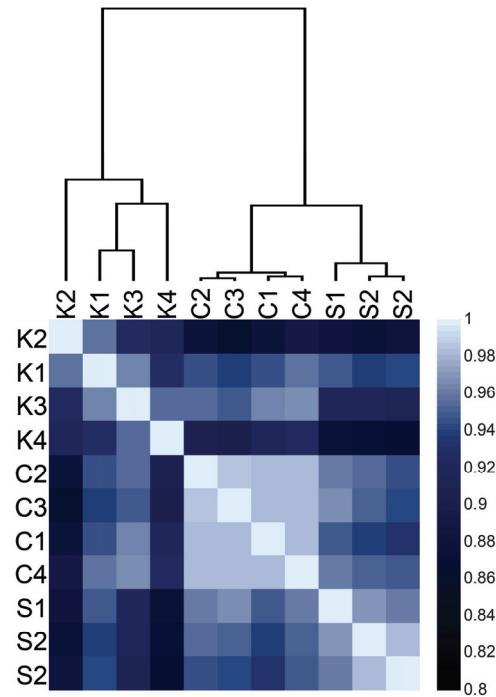
(b) Autoradiographs of CLIP-seq experiments performed in parallel using two different antibodies, a commercially available rabbit polyclonal TDP-43 antibody (Aviva Systems Biology, Cat. No. ARP38942_T100) left and an in-house monoclonal antibody recognizing an epitope within amino acids 251-414 of human TDP-43¹⁶. Under identical conditions and exposure times, our monoclonal antibody showed a much higher potency of immunoprecipitating TDP-43-RNA complexes. The orange box depicts the excised low mobility complexes used for the cDNA libraries for comparison to the monomeric TDP-43 complexes. (c) Flow-chart illustrating the number of reads sequenced and aligned from the two independent CLIP-seq experiments. CLIP-seq libraries were subjected to 36-bp sequencing on the Illumina Genome Analyzer 2. In total 1 and 4.5 million reads were mapped uniquely to annotated genes for experiment 1 and 2 respectively. (d) Reproducibility of CLIP-seq experiments on a genome-wide scale. Clusters identified in independent CLIP-seq experiments were considered to overlap if 1 base of a cluster in one experiment extended to a cluster in the other experiment (left panel). A gene containing an overlapping cluster was considered to overlap (right panel). Venn diagrams revealed statistically significant overlap between clusters and genes in replicate CLIP-seq libraries, with randomly distributed clusters shown as a comparison (lower panel). (e) Gene target saturation chart plotting gene targets found by cluster-finding on increasing sampling rates (5% intervals). Data follows a logarithmic expansion with an R² value of 0.98.



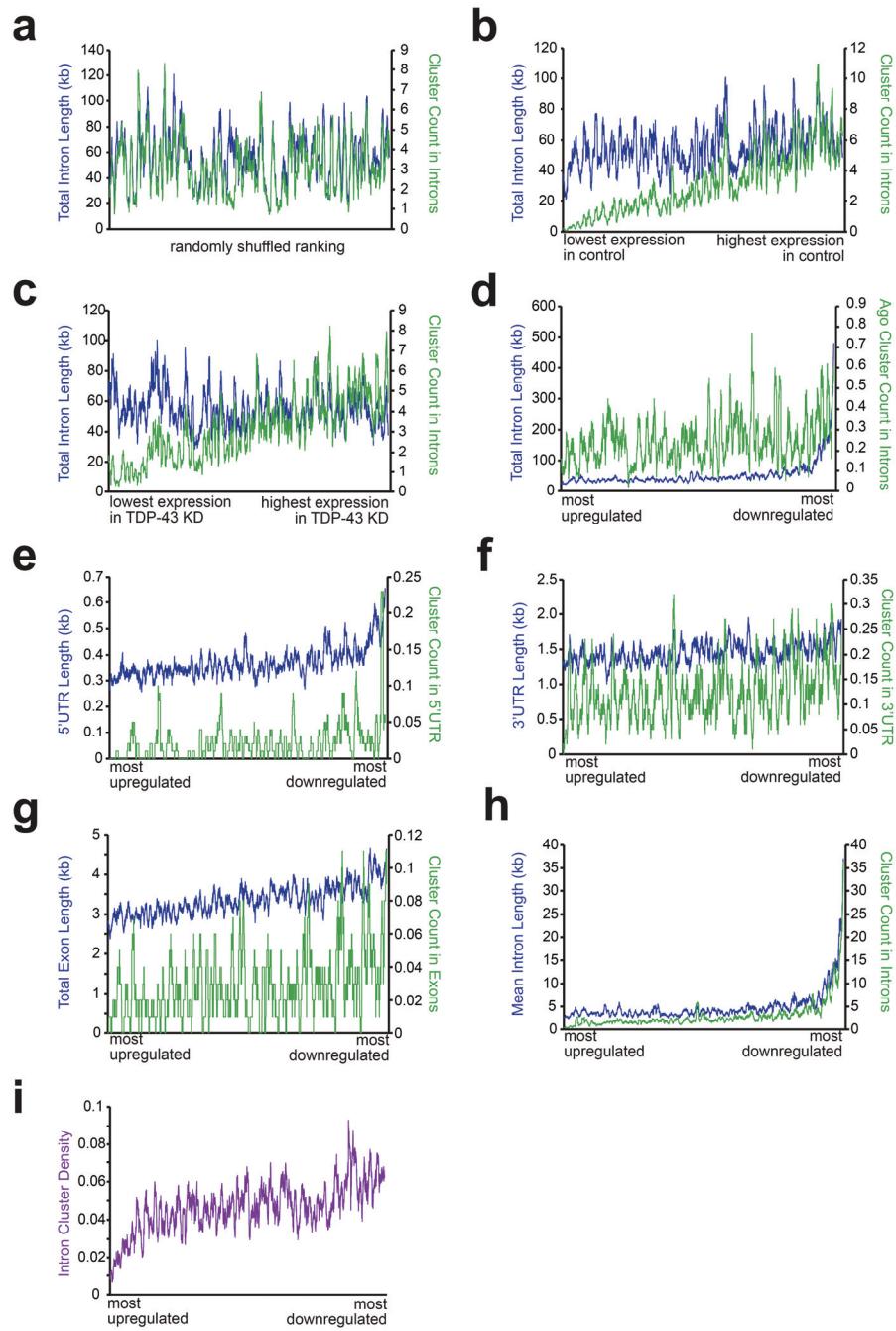


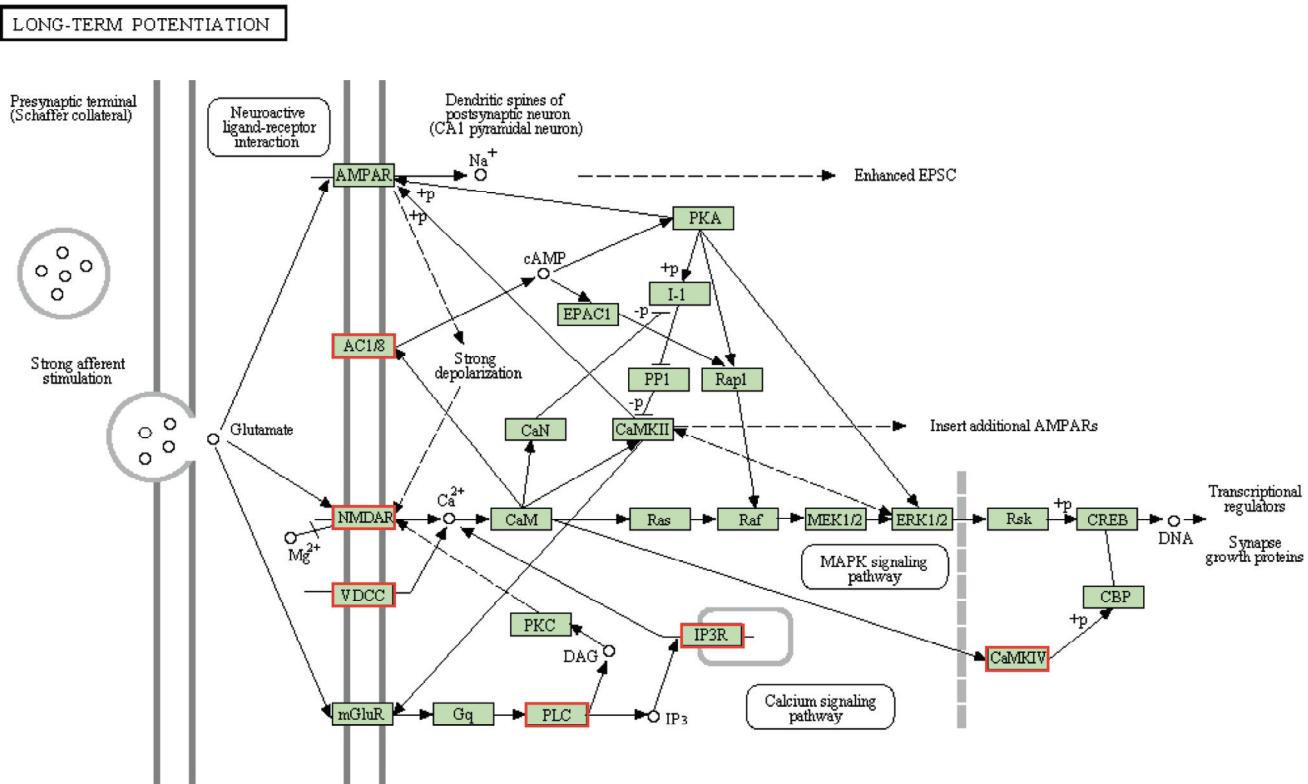
Supplementary Figure 2 Cluster strength and gene-location biases of TDP-43 binding. **(a)** Box plots of cluster strength (by χ^2 analysis) versus GUGU-cluster bins (counts of non-overlapping GUGU tetramer found within the cluster). By *t*-test comparison to all clusters, bins of 11-15 and 16+ GUGUs were significantly enriched ($p < 0.01$ and $p < 10^{-37}$, respectively). On each box, the central mark is the median, the edges of the box are the 25th and 75th percentiles, the whiskers extend to the most extreme data points not considered outliers, and outliers are plotted individually **(b)** Pre-mRNAs were divided into annotated 5' and 3' untranslated regions, exons, proximal introns (<0.5kb from a splice junction), distal introns (>0.5kb from a splice junction) and unannotated regions. Pie-charts revealed that the majority of TDP-43 binding sites were located in distal intronic regions of pre-mRNA (left panel). For comparison, previously published Argonaute (Ago) binding sites in mouse brain²¹ are displayed as analogous pie-charts (right panel). **(c)** CLIP binding sites of TDP-43 in the two replicates, Ago, and random TDP-43 clusters across genes. The fraction of CLIP clusters was plotted depending on the relative gene position from the 5' to the 3' ends of each target gene.

Supplementary Figure 3 RNA-seq biological replicas. Correlation between RNA-seq results obtained from mice subjected to different ASO treatments. Heatmap generated from Cluster3 and Matlab, using linear least-squares regression correlation coefficients of the pair-wise comparison between RPKM values of all genes from each experiment. “K” is TDP-43 knockdown samples, “C” is control oligo-, “S” is saline-treated samples, and numbers represent biological replicates.



Supplementary Figure 4 Correlation between RNA-seq and CLIP-seq data using various parameters. **(a)** Genes were ranked randomly instead of upon their degree of regulation after TDP-43 depletion and the average TDP-43 CLIP clusters found in introns of the next 100 genes in the ranked list were plotted (green line). Similarly, the median of total intron length for the next 100 genes was plotted (blue line). **(b)** Genes were ranked by ascending expression (RPKM) values in the samples treated with control ASO. **(c)** Genes were ranked by ascending expression (RPKM) values in the samples treated with TDP-43 ASO. **(d)** Genes were ranked upon their degree of regulation after TDP-43 depletion and average Ago clusters found in introns of the next 100 genes (green line) or the total intron length for the next 100 genes (blue line) were plotted. **(e)** Genes were ranked upon their degree of regulation after TDP-43 depletion and average clusters found in 5'UTR for the next 100 genes (green line) or the total 5'UTR length for the next 100 genes (blue line) were plotted. **(f)** Genes were ranked upon their degree of regulation after TDP-43 depletion and average clusters found in 3'UTR for the next 100 genes (green line) or the total 3'UTR length for the next 100 genes (blue line) were plotted. **(g)** Genes were ranked upon their degree of regulation after TDP-43 depletion and average clusters found in exons for the next 100 genes (green line) or the total exon length for the next 100 genes (blue line) were plotted. No correlation between CLIP and RNA-seq data was observed **(a-f)**. **(h)** Genes were ranked upon their degree of regulation after TDP-43 depletion and average clusters found in introns for the next 100 genes (green line) or the average intron length for the next 100 genes (blue line) were plotted. **(i)** Genes were ranked upon their degree of regulation after TDP-43 depletion and average cluster density (cluster count/intron length) for the next 100 genes was plotted.

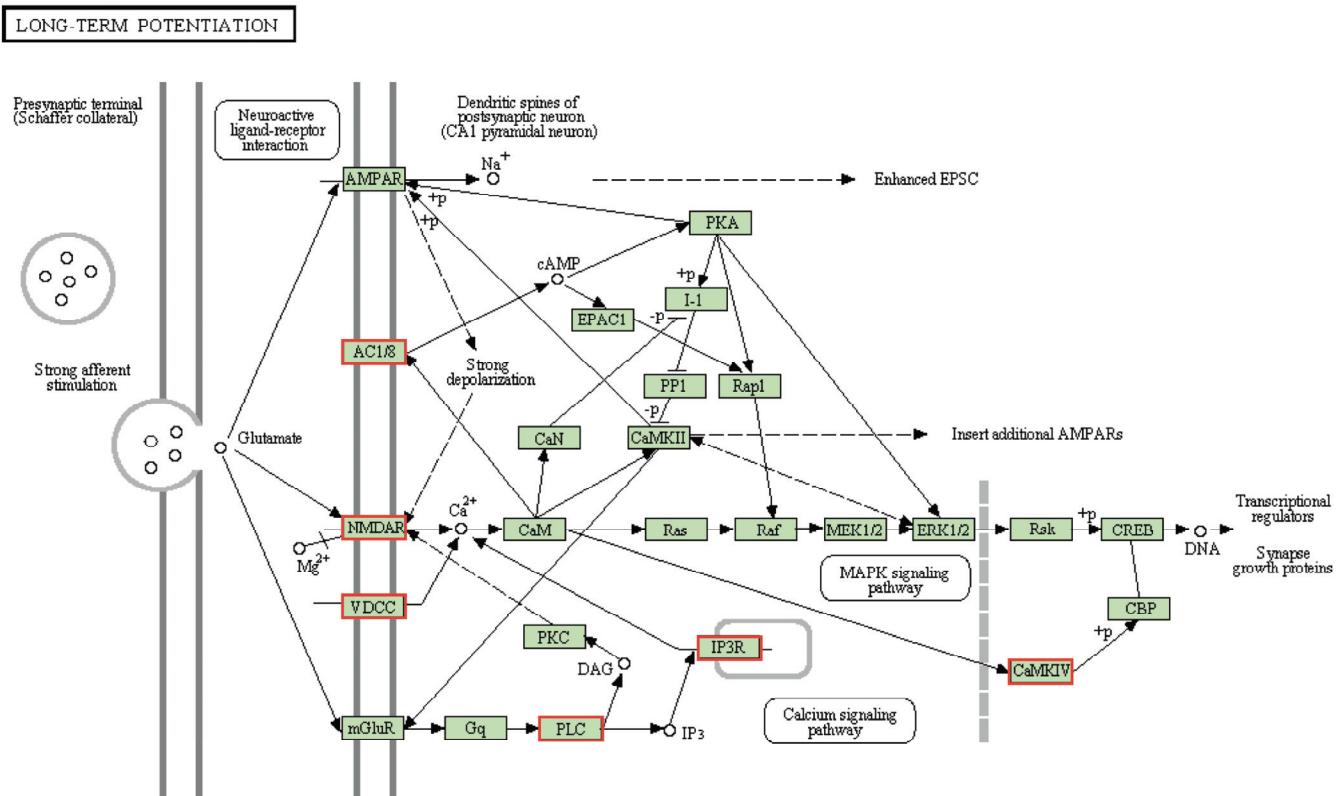


a**b**

Downregulated TDP-43 targets found in the long-term potentiation pathway

Gene Symbol	Gene name	Ratio KD/Ctrl
<i>Adcy1</i>	Adenylate cyclase 1	0.56
<i>Cacna1C</i>	Calcium channel, voltage dependent, L type, alpha 1C subunit	0.58
<i>Camk4</i>	Calcium/calmodulin-dependent protein kinase	0.59
<i>Grin2c</i>	Glutamate receptor, ionotropic, NMDA2C (epsilon 3)	0.63
<i>Itp1</i>	Inositol 1,4,5-triphosphate receptor 1	0.63
<i>Plcb1</i>	Phospholipase C, beta 1	0.56
<i>Grin2a</i>	similar to NMDA receptor channel subunit epsilon 1, glutamate receptor ionotropic	0.52

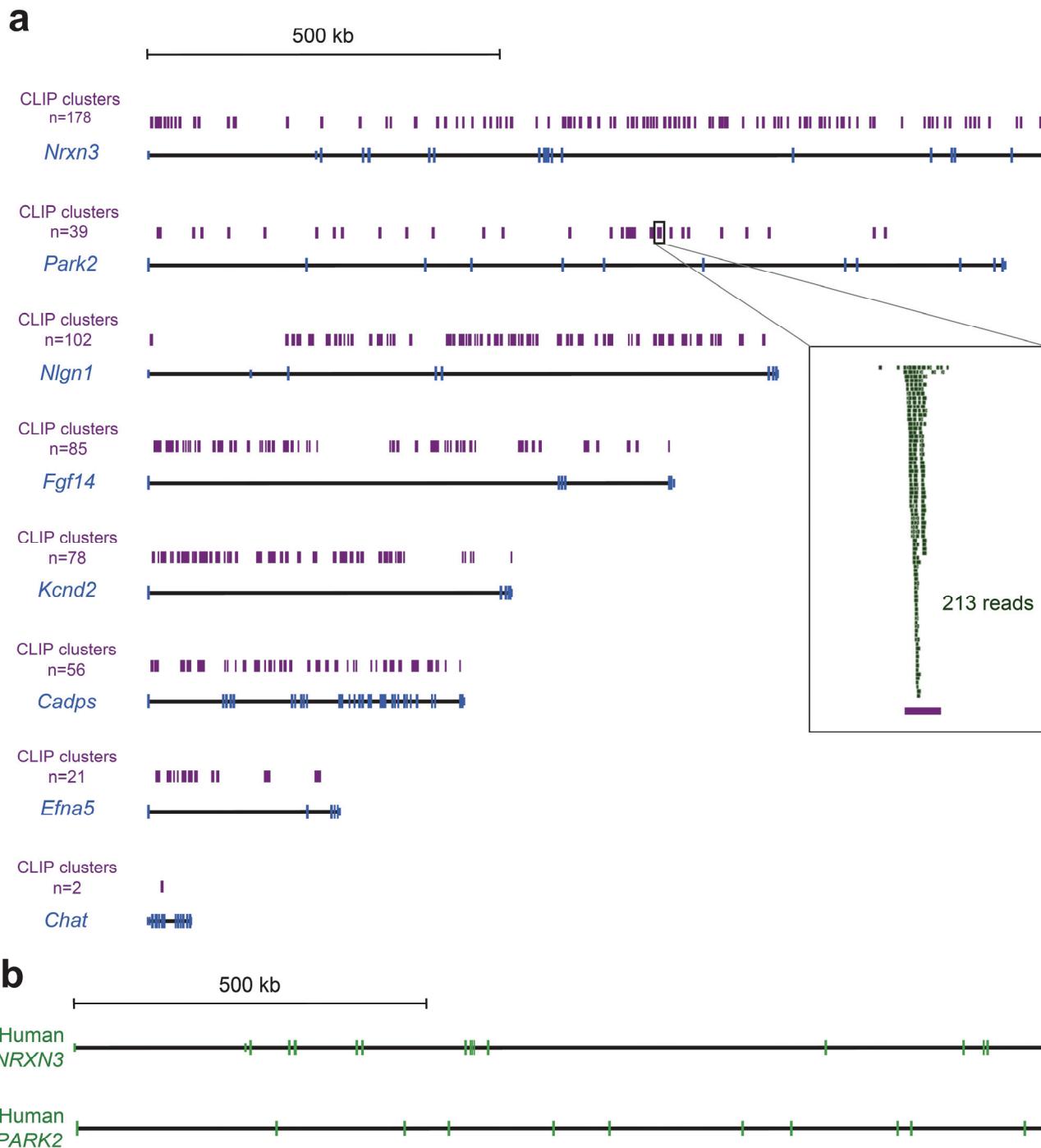
Supplementary Figure 5 The calcium signaling pathway is affected by TDP-43 depletion. **(a)** The calcium-signaling pathway annotated by KEGG (Kyoto Encyclopedia of Genes and Genomes) was found to be significant using the functional annotation tool DAVID. Red-bordered gene groups contain TDP-43 targets that are downregulated upon TDP-43 depletion. **(b)** List of downregulated TDP-43 targets contributing to calcium-signaling pathway

a**b**

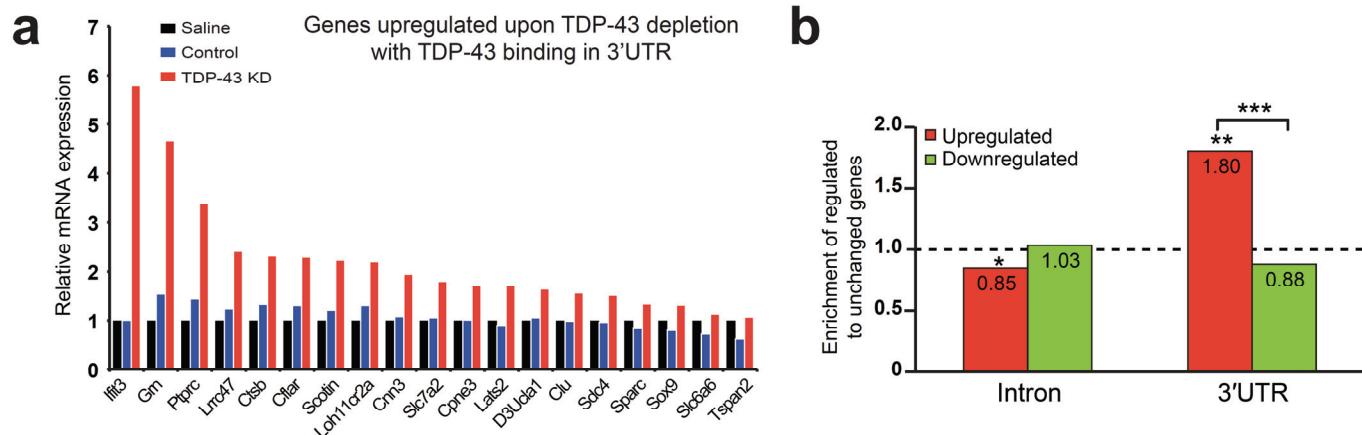
Downregulated TDP-43 targets found in the long-term potentiation pathway

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<i>Itpr1</i>	Inositol 1,4,5-triphosphate receptor 1	0.63
<i>Plcb1</i>	Phospholipase C, beta 1	0.56
<i>Grin2a</i>	similar to NMDA receptor channel subunit epsilon 1, glutamate receptor ionotropic	0.52

Supplementary Figure 6 The long-term potentiation pathway is affected by TDP-43 depletion. **(a)** The long-term potentiation pathway annotated by KEGG was found to be significant using the functional annotation tool DAVID. Red-bordered gene groups contain TDP-43 targets that are downregulated upon TDP-43 depletion. **(b)** List of downregulated TDP-43 targets contributing to long-term potentiation pathway.

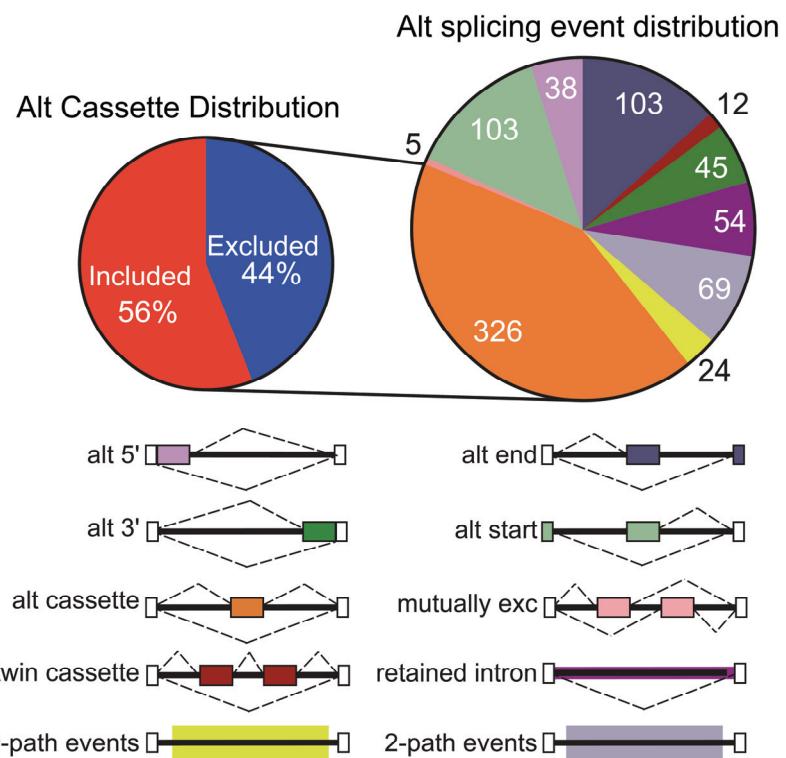


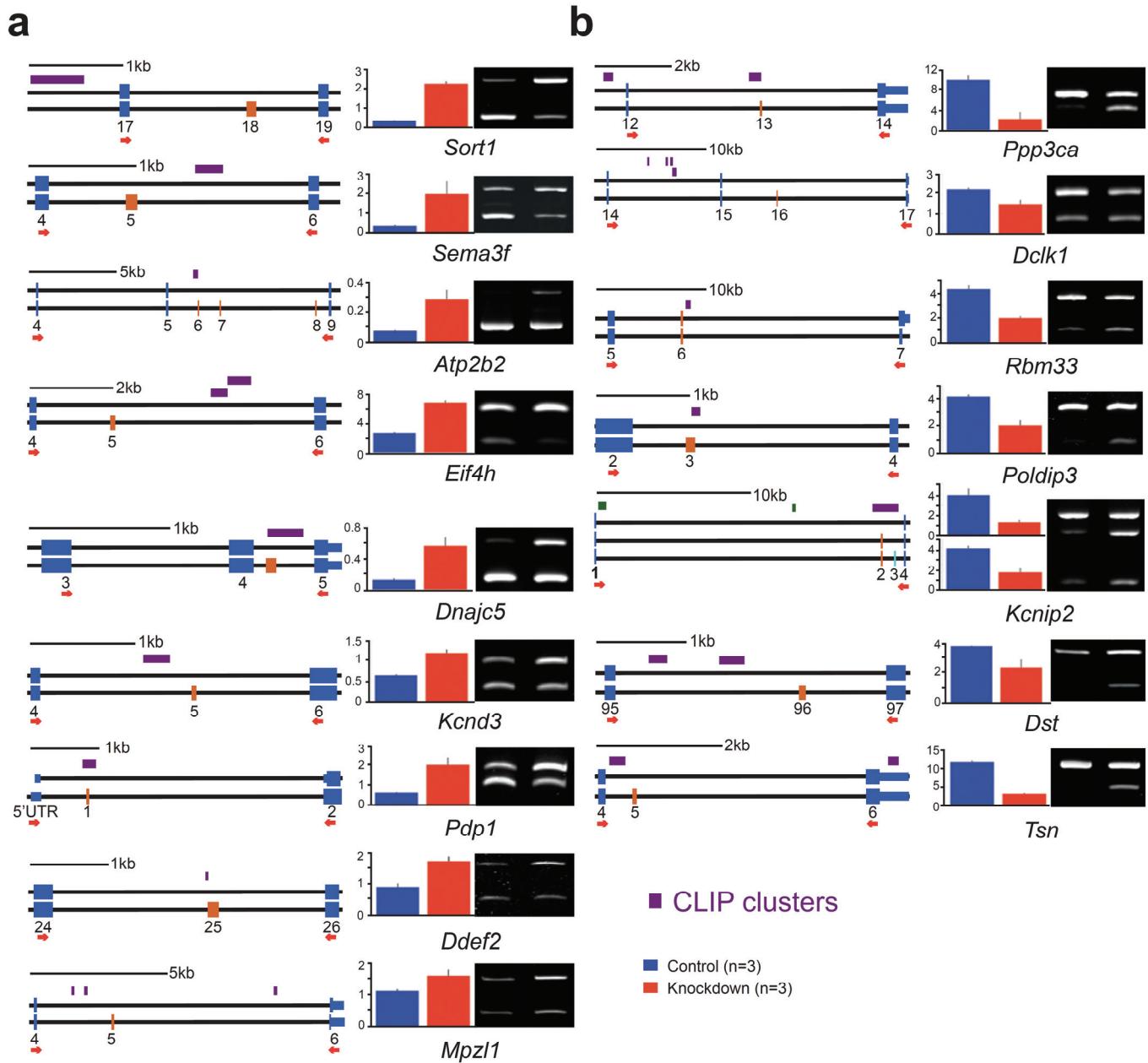
Supplementary Figure 7 Representative examples of genes with long introns and multiple TDP-43 binding sites. **(a)** Most transcripts in this group (mean intron length >10kb) displayed multiple intronic TDP-43 binding sites as determined by CLIP-seq (purple bars above each gene). In contrast, *Chat* is an example of a downregulated gene with short intron length (mean intron length <10kb) that shows a single TDP-43 binding site. The number of clusters per gene (n) is in purple on the left. Note that each cluster represents a binding cluster defined by a collection of overlapping reads as shown for *Park2* (inset). **(b)** Examples of conservation of gene structures in human neurexin 3 and parkin 2 showing similar genic architectures as their mouse orthologues.



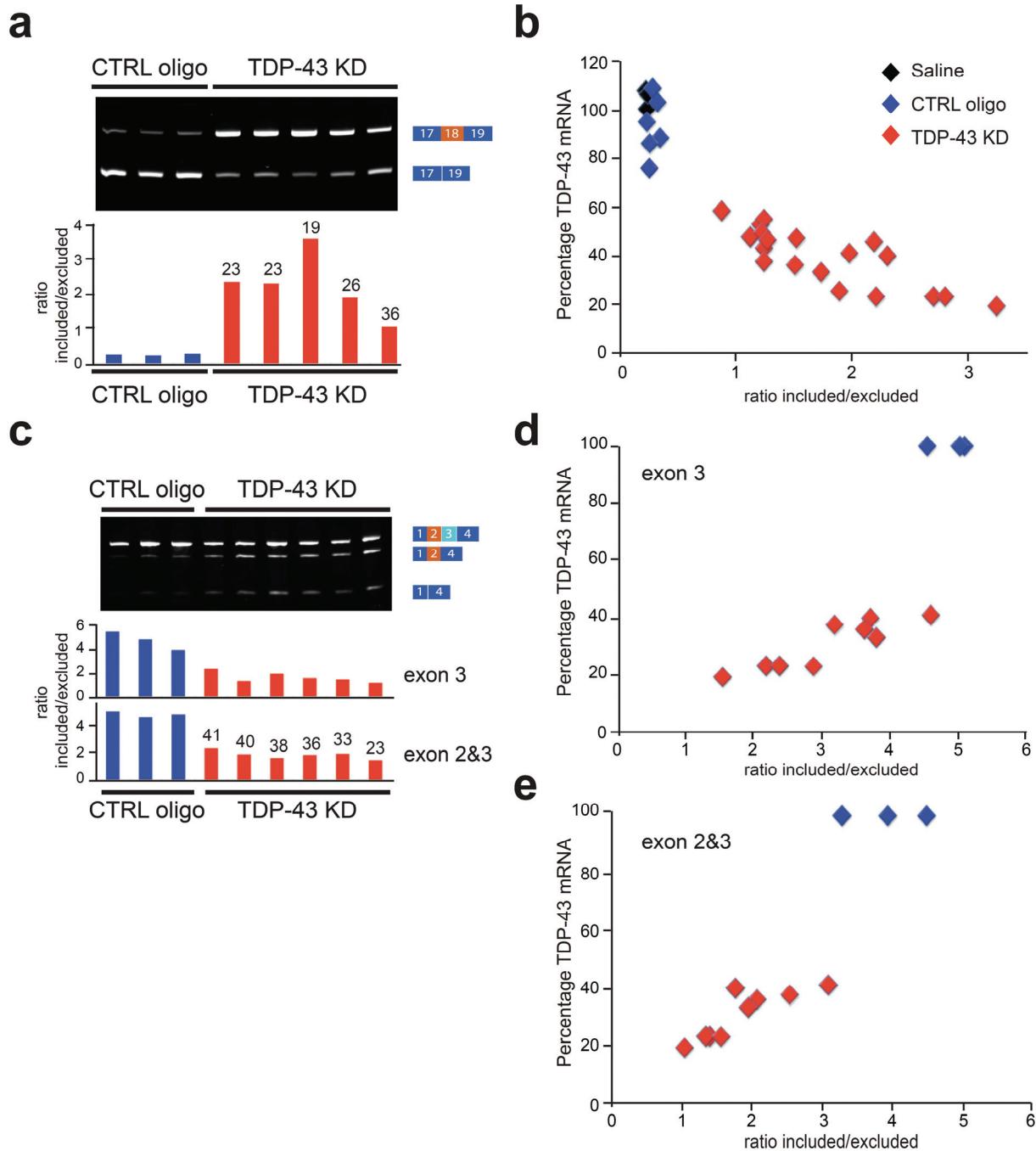
Supplementary Figure 8 TDP-43 binding on the 3'UTR of RNAs represses gene expression. (a) Normalized expression (based on RPKM values from RNA-seq) of selected up-regulated genes upon TDP-43 depletion that also contain TDP-43 binding regions in their 3'UTR. (b) Enrichment for binding within the 3'UTR among upregulated TDP-43 targets, compared to unchanged genes. *Upregulated with intronic binding versus unchanged with intronic binding ($p < 1.8 \times 10^{-6}$), **Upregulated with 3'UTR binding versus unchanged with 3'UTR binding ($p < 8.2 \times 10^{-3}$), ***Upregulated with 3'UTR binding versus downregulated with 3'UTR binding ($p < 1.4 \times 10^{-2}$). P-values calculated by chi-square.

Supplementary Figure 9 Splicing changes upon TDP-43 depletion identified by exon-junction arrays. Distribution of alternative splicing events upon TDP-43 depletion detected using splicing-sensitive microarrays. Of the 326 cassette events defined by Affymetrix on mm9 annotation, 287 were annotated by our stringent gene structure annotations in mm8, and were used for comparisons to RNA-seq and CLIP-seq data.

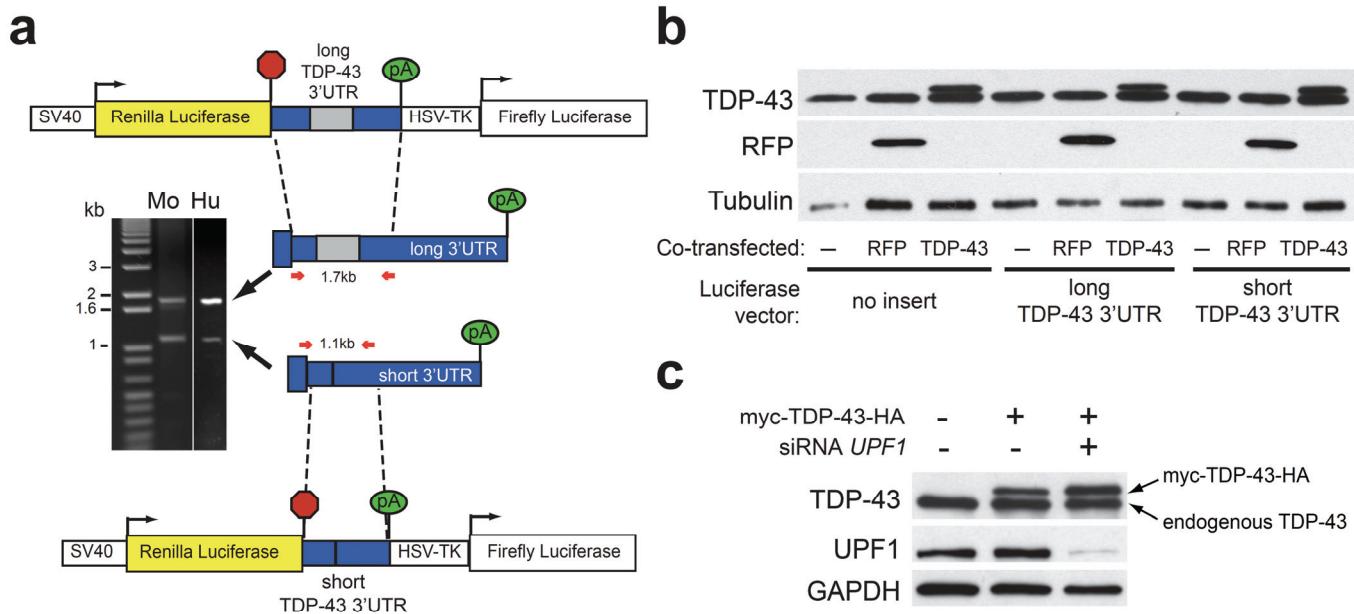




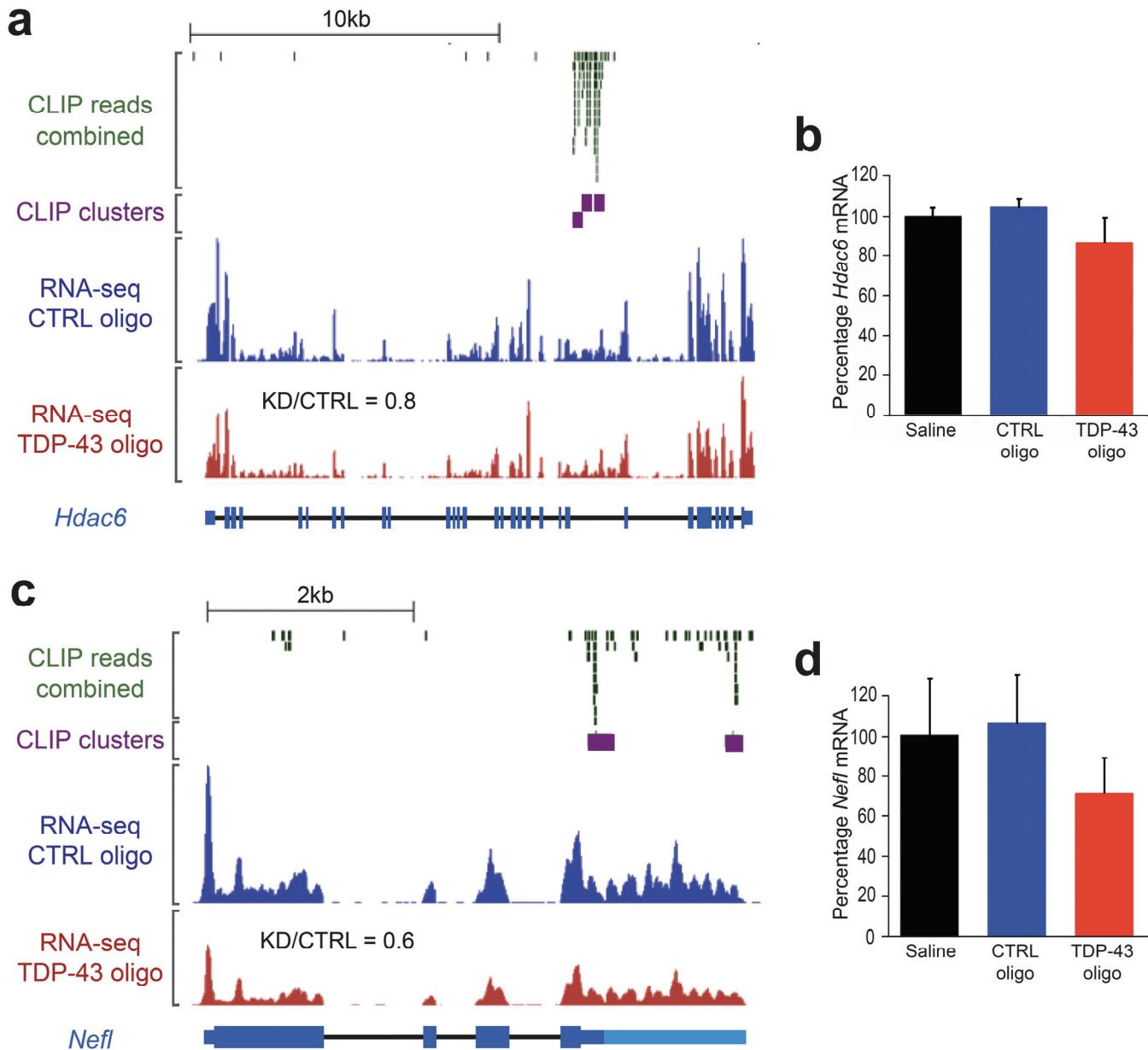
Supplementary Figure 10 Examples of alternative splicing regulation by TDP-43. RNA targets with exons included (a) or excluded (b) upon TDP-43 knockdown (same as in Fig. 4d). Semi-quantitative RT-PCR of selected targets showing splice changes in samples with TDP-43 knockdown compared to controls. Schematic representation of assessed exons with the changed exon(s) colored orange (left). The exon number of the gene is indicated below each box. The red arrows depict the position of the primers used for RT-PCR. Purple boxes indicate TDP-43 binding sites as defined by CLIP-seq. Representative acrylamide gel pictures of RT-PCR products from control or knockdown adult brain samples, as indicated (right panel). Quantification of splicing changes from three biological replicas per group is shown in the middle panel.



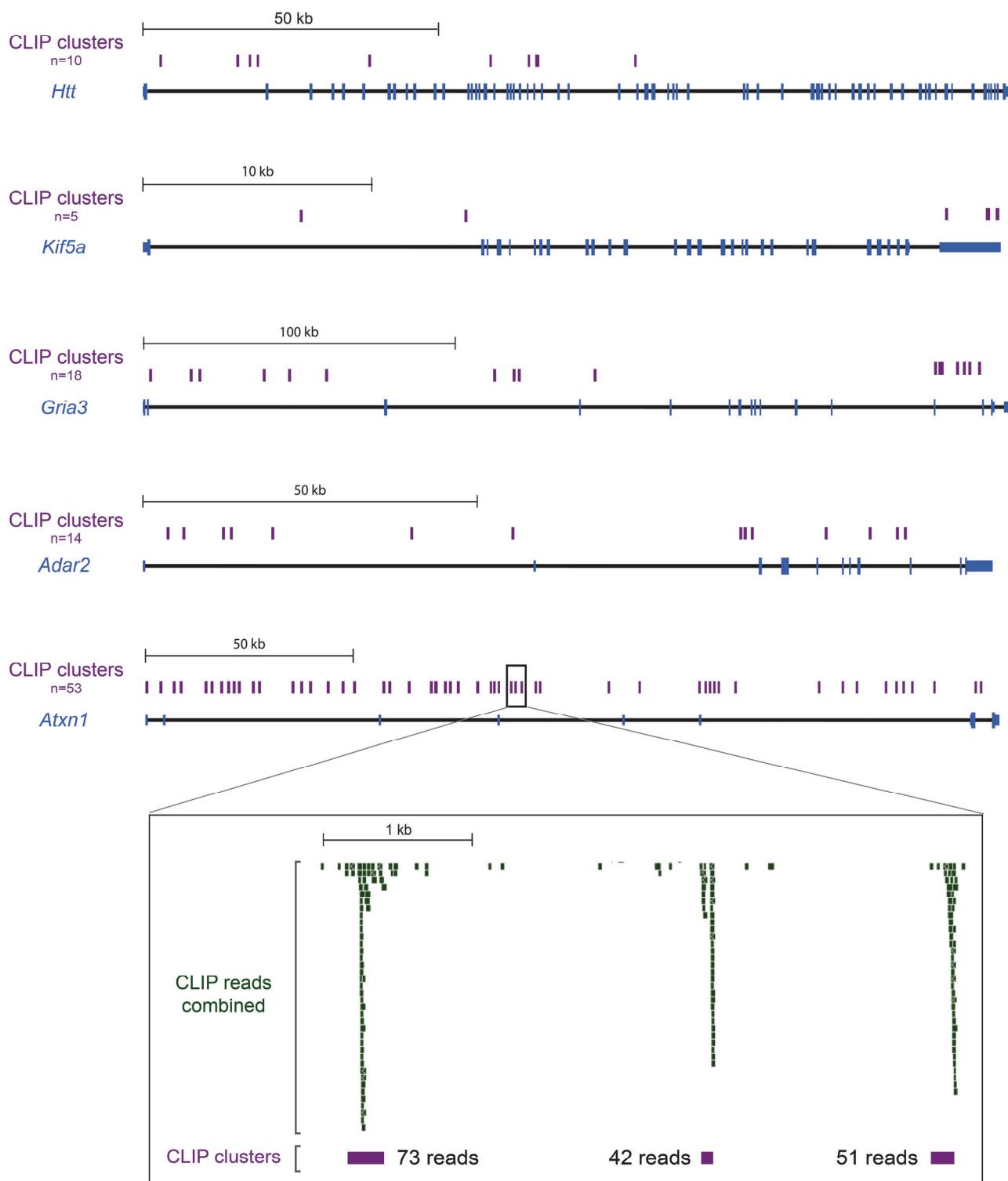
Supplementary Figure 11 Splicing changes correlate with the level of TDP-43 knockdown. **(a)** Acrylamide gels with semi-quantitative RT-PCR samples showing sortilin 1 (*Sort1*) splicing changes in mice with various levels of TDP-43 reduction (shown as percentages above each bar). **(b)** Significant correlation of TDP-43 levels to *Sort1* splicing changes (correlation value = -0.905, n=27). **(c)** Acrylamide gels with semi-quantitative RT-PCR samples showing *Kcnip* splicing changes in mice with various levels of TDP-43 reduction (shown as percentages above each bar on the lowest panel). **(D-E)** Significant correlation of TDP-43 levels to *Kcnip* splicing changes (correlation value = 0.91 for exon 3 and 0.83 for exon 2 and 3, n=12).



Supplementary Figure 12 TDP-43 3'UTRs used in luciferase assays and control immunoblots. **(a)** Two alternative 3'UTRs of TDP-43 were amplified from mouse or human cDNA using primers whose approximate locations are shown by the small red arrows below the schemes on the right. The first 1.7kb or 1.1kb of each long (unspliced) or short (spliced) 3'UTR respectively were then cloned into a renilla luciferase reporter vector. The latter also contains the firefly luciferase gene that is expressed independently from renilla luciferase and serves as a transfection normalization control. **(b)** Representative immunoblots of HeLa cell lysates used for luciferase assays in **Fig. 5F** showing increased expression of TDP-43 in samples transfected with a *myc-hTDP-43-HA* expressing vector. For control, cells were transfected with a vector expressing an unrelated protein, namely red fluorescence protein (RFP), whose levels were confirmed by immunoblot (second panel). **(c)** Representative immunoblots of HeLa cell lysates used for **Fig. 5F,G** showing decreased levels of *UPF1* in samples transfected with *UPF1* siRNA.



Supplementary Figure 13 TDP-43 binding and regulation of *H dac6* and *Nefl* transcripts. **(a)** CLIP-seq reads and clusters on *H dac6* transcript showing intronic TDP-43 binding. RNA-seq reads from control or TDP-43 knockdown samples (equal scales) show a slight decrease in *H dac6* mRNA in the TDP-43 knockdown group. **(b)** Quantitative RT-PCR confirmed the slight decrease in *H dac6* mRNA upon TDP-43 depletion. Standard deviation was calculated within each group for 3 biological replicates. **(c)** CLIP-seq reads and clusters on *Nefl* mRNA showing two distinct TDP-43 binding sites within the 3'UTR. Our RNA-seq reads indicate that the 3'UTR of mouse *Nefl* is longer than reported in UCSC database (light blue bar indicates the extention). RNA-seq reads from control or TDP-43 knockdown samples show a slight decrease in *Nefl* mRNA in the TDP-43 knockdown group, in accordance with previous report.



Supplementary Figure 14 TDP-43 binding patterns on transcripts encoding for selected disease-related proteins. The number of clusters per gene (n) is in purple on the left. Note that each cluster represents a binding site defined by a collection of overlapping reads as shown for ataxin 1 (inset).

Supplementary Table 1 Genes upregulated upon TDP-43 depletion in adult mouse brain

Gene symbol	Protein	Refseq/mRNA identifier	Number of CLIP-seq clusters					RNA-seq		
			Total	in 5'UTR	in introns	in exons	in 3'UTR	RPKM in TDP-43 KD	RPKM in control	Ratio KD/control
Oas12	Oas12 protein	BC034361	0	0	0	0	0	29.97	2.86	10.49
Iif1	Interferon-induced protein with tetratricopeptide repeats 1 (IIFIT-1)	NM_008331	0	0	0	0	0	23.26	2.11	11.03
Iif3	Interferon-induced protein with tetratricopeptide repeats 3 (IIFIT-3)	NM_010501	0	0	0	0	0	20.03	3.07	6.53
Bst2	DAMP-1 protein	NM_198095	0	0	0	0	0	16.05	3.21	5.00
5830458K16Rik	Receptor transporting protein 4	NM_023386	0	0	0	0	0	10.03	1.44	6.98
Stat1	Signal transducer and activator of transcription 1	AK046517	0	0	0	0	0	20.59	4.52	4.56
Gpnmb	Glycoprotein (transmembrane) nmb	AK079220	0	0	0	0	0	70.72	16.86	4.20
Lgals3bp	Lectin, galactoside-binding, soluble, 3 binding	NM_011150	0	0	0	0	0	73.81	17.96	4.11
Iifm3	Interferon induced transmembrane protein 3	NM_025378	0	0	0	0	0	30.74	8.52	3.61
Tagln2	Transgelin 2	BC049861	0	0	0	0	0	15.17	3.62	4.19
Iif3	Interferon-induced protein with tetratricopeptide repeats 3 (IIFIT-3)	AK077243	1	0	0	0	1	9.91	1.72	5.75
Irgm	Interferon inducible protein 1	AK002545	0	0	0	0	0	14.53	3.68	3.95
Vim	Vimentin	NM_011701	0	0	0	0	0	111.40	31.33	3.56
C3	Complement component 3	NM_009778	0	0	0	0	0	8.71	1.57	5.56
Gbp2	Guanylate nucleotide binding protein 2	NM_010260	0	0	0	0	0	7.49	1.33	5.61
Cd5l	CD5 antigen-like	NM_009690	0	0	0	0	0	6.39	0.98	6.50
Cd44	CD44 antigen isoform b	NM_001039150	0	0	0	0	0	12.36	2.87	4.30
Serpina1	Serine (or cysteine) proteinase inhibitor, clade	NM_009776	0	0	0	0	0	14.77	3.96	3.73
C3ar1	Complement component 3a receptor 1	NM_009779	0	0	0	0	0	16.68	4.72	3.53
Trim30	Tripartite motif protein 30 (Down regulatory protein of interleukin 2 receptor)	AF220014	0	0	0	0	0	8.96	1.91	4.69
Cybb	Cytochrome b-245, beta polypeptide	NM_007807	0	0	0	0	0	5.49	0.86	6.36
Cd84	CD84 antigen	AK171067	0	0	0	0	0	22.69	7.54	3.01
A2m	Alpha-2-macroglobulin	NM_175628	0	0	0	0	0	11.32	2.76	4.10
Iif27	Interferon stimulated gene 12(b1)	NM_029803	0	0	0	0	0	4.29	0.55	7.76
Grn	Granulin	NM_008175	1	0	0	0	1	70.17	23.12	3.04
Fbxo39	Novel TRAF-type zinc finger protein	AK046736	0	0	0	0	0	11.26	2.78	4.05
Ccnd1	Cyclin D1	NM_007631	0	0	0	0	0	33.11	11.12	2.98
Lgals3	Galectin 3	NM_010705	0	0	0	0	0	12.07	3.31	3.65
Cdkn1a	Cyclin-dependent kinase inhibitor 1A	NM_007669	1	0	1	0	0	26.03	9.17	2.84
Usp18	Ubiquitin specific protease 18	NM_011909	0	0	0	0	0	4.11	0.57	7.25
Gbp1	Guanylate nucleotide binding protein 1	NM_012059	0	0	0	0	0	6.55	1.40	4.67
Eif2ak2	Protein kinase, interferon-inducible double	NM_011163	0	0	0	0	0	11.99	3.26	3.68
Apoebc1	Apolipoprotein B mRNA editing enzyme	BC003792	0	0	0	0	0	11.28	2.94	3.84
Spp1	Secreted phosphoprotein 1	NM_009263	0	0	0	0	0	35.34	12.35	2.86
Tyrobp	TYRO protein tyrosine kinase binding protein	NM_011662	0	0	0	0	0	37.90	13.18	2.87
Lgals9	Lectin, galactose binding, soluble 9	NM_010708	0	0	0	0	0	16.47	5.34	3.09
Sifn8	Schlafchen 8	NM_181545	0	0	0	0	0	5.31	0.97	5.45
Cst7	Cystatin F (leukocystatin)	NM_009977	0	0	0	0	0	12.31	3.60	3.42
Igf1	Insulin-like growth factor I precursor (IGF-I) (Somatomedin)	AY878193	0	0	0	0	0	7.26	1.73	4.20
Tgm1	Transglutaminase 1, K polypeptide	NM_019984	0	0	0	0	0	4.50	0.69	6.48
Fcer1g	Fc receptor, IgE, high affinity I, gamma	NM_010185	0	0	0	0	0	33.93	12.36	2.75
Ddx58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	AK155930	0	0	0	0	0	6.74	1.66	4.07
Isgr3q	Interferon dependent positive acting	NM_008394	0	0	0	0	0	15.30	5.00	3.06
C1qa	Complement component 1, q subcomponent, A chain	NM_007572	0	0	0	0	0	137.39	50.81	2.70
H2-K1	H2-K1 protein	BC080756	0	0	0	0	0	31.08	11.60	2.68
Parp9	B aggressive lymphoma	NM_030253	0	0	0	0	0	6.64	1.68	3.94
Cd52	CD52 antigen	NM_013706	0	0	0	0	0	10.40	2.87	3.62
H2-D1	H-2 class I histocompatibility antigen, D-B alpha chain precursor (H-2D(B))	AK159572	0	0	0	0	0	44.59	16.67	2.67
Cd68	Macrosialin precursor (CD68 antigen)	BC021637	0	0	0	0	0	38.54	14.73	2.62
S100a6	S100 calcium binding protein A6 (calcyclin)	NM_011313	0	0	0	0	0	11.39	3.44	3.31
Rsad2	Viral hemorrhagic septicemia virus(VHSV) induced	NM_021384	0	0	0	0	0	4.28	0.70	6.12
B2m	Beta-2-microglobulin	NM_009735	0	0	0	0	0	139.63	54.00	2.59
Fcgr2b	Low affinity immunoglobulin gamma Fc region receptor II precursor	NM_010187	0	0	0	0	0	11.96	3.85	3.11
Sifn2	Schlafchen 2	NM_011408	0	0	0	0	0	7.60	2.09	3.64
Arpc1b	Actin related protein 2/3 complex, subunit 1B	AK171364	0	0	0	0	0	11.69	3.81	3.07
ligrp2	Highly similar to Mus musculus interferon-gamma induced GTPase	AK128991	0	0	0	0	0	8.11	2.26	3.59
Ly9	Ly9 protein	BC095921	0	0	0	0	0	9.30	2.77	3.37
Sn	Sialoadhesin	NM_011426	0	0	0	0	0	3.25	0.55	5.88
Sifn9	Schlafchen 9	NM_172796	0	0	0	0	0	3.48	0.60	5.81
Dtx3l	Weakly similar to B-lymphoma- and BAL-associated protein (Rhysin 2)	BC085093	0	0	0	0	0	8.50	2.56	3.32
NM_205820	Toll-like receptor 13	NM_205820	0	0	0	0	0	7.47	2.23	3.36
Lyzs	Lysozyme C type M precursor	AK159276	0	0	0	0	0	111.97	46.71	2.40
Cxcr4	C-X-C chemokine receptor type 4	NM_009911	0	0	0	0	0	6.74	1.94	3.47
Sifn5	Schlafchen 5	NM_183201	0	0	0	0	0	8.63	2.60	3.32
Msn	Moesin	NM_010833	0	0	0	0	0	33.37	14.04	2.38
Lilrb4	Leukocyte immunoglobulin-like receptor, Poly (ADP-ribose) polymerase family, member 14	NM_013532	0	0	0	0	0	5.25	1.29	4.07
Parp14	Poly (ADP-ribose) polymerase family, member 14	NM_001039530	0	0	0	0	0	6.08	1.65	3.70
Cd48	CD48 antigen	NM_007649	0	0	0	0	0	8.11	2.49	3.26

<i>Edg3</i>	Endothelial differentiation, sphingolipid	NM_010101	0	0	0	0	0	10.24	3.29	3.11	4.03
<i>Laptm5</i>	Lysosomal-associated protein transmembrane 5	NM_010686	0	0	0	0	0	53.57	23.32	2.30	4.03
<i>Msr2</i>	Macrophage scavenger receptor 2	NM_030707	0	0	0	0	0	60.70	25.61	2.37	4.00
<i>Creg1</i>	Cellular repressor of E1A-stimulated genes 1	NM_011804	0	0	0	0	0	25.09	11.02	2.28	3.99
<i>Emp1</i>	Epithelial membrane protein 1	NM_010128	0	0	0	0	0	5.99	1.59	3.76	3.99
<i>Hmox1</i>	Heme oxygenase (decycling) 1	NM_010442	0	0	0	0	0	12.84	4.95	2.60	3.96
<i>Zbtb20</i>	Zinc finger protein 288	BC056446	27	0	27	0	0	10.94	3.79	2.89	3.95
<i>Trem2</i>	Triggering receptor expressed on myeloid cells	NM_031254	0	0	0	0	0	46.13	19.85	2.32	3.92
<i>Cd53</i>	CD53 antigen	NM_007651	0	0	0	0	0	20.62	9.15	2.25	3.84
<i>Ang1</i>	Angiogenin, ribonuclease A family, member 1	NM_007447	0	0	0	0	0	21.94	9.78	2.24	3.79
<i>Ms4a7</i>	MS4A7 protein homolog	AK079888	0	0	0	0	0	5.29	1.41	3.74	3.78
<i>Abca1</i>	ATP-binding cassette sub-family A member 1	NM_013454	6	0	6	0	0	32.69	14.78	2.21	3.73
<i>Ctsz</i>	Cathepsin Z proprotein	NM_022325	0	0	0	0	0	55.45	25.30	2.19	3.73
<i>Slc43a3</i>	E030016B05 product:embryonic epithelial gene 1	AK086962	0	0	0	0	0	4.91	1.29	3.82	3.73
<i>Al451617</i>	Hypothetical protein LOC209387	NM_199146	0	0	0	0	0	4.37	1.02	4.28	3.72
<i>Tap1</i>	Transporter 1, ATP-binding cassette, subfamily	NM_013683	0	0	0	0	0	4.36	1.03	4.22	3.68
<i>Ctsd</i>	Cathepsin D	AK152638	2	0	2	0	0	333.96	152.95	2.18	3.68
<i>Osmr</i>	Oncostatin M receptor beta	AB015978	0	0	0	0	0	8.11	2.73	2.97	3.67
<i>Cd300lf</i>	Polymeric immunoglobulin receptor 3	AF251703	0	0	0	0	0	3.16	0.65	4.86	3.67
<i>Cyba</i>	Cytochrome b-245, alpha polypeptide	NM_007806	0	0	0	0	0	12.34	4.92	2.51	3.67
<i>Tapbp</i>	TAP binding protein isoform 1	NM_001025313	0	0	0	0	0	18.91	8.34	2.27	3.66
<i>C1qb</i>	Complement component 1, q subcomponent, B chain	NM_009777	2	0	2	0	0	110.40	50.84	2.17	3.65
<i>Cd180</i>	CD180 antigen	NM_008533	0	0	0	0	0	9.19	3.20	2.87	3.63
<i>Ifi2</i>	Interferon-induced protein with	NM_008332	0	0	0	0	0	9.25	3.26	2.84	3.61
<i>Lgals1</i>	Lectin, galactose binding, soluble 1	NM_008495	0	0	0	0	0	9.55	3.44	2.77	3.56
<i>Gfap</i>	Glia fibrillary acidic protein	AK140151	0	0	0	0	0	98.80	46.64	2.12	3.54
<i>Ifih1</i>	Melanoma differentiation associated protein-5	NM_027835	0	0	0	0	0	5.25	1.57	3.35	3.53
<i>Tmem106a</i>	Hypothetical protein LOC217203	NM_144830	0	0	0	0	0	4.01	0.94	4.25	3.52
<i>Cxcl5</i>	Chemokine (C-X-C motif) ligand 5	NM_009141	0	0	0	0	0	2.79	0.60	4.63	3.49
<i>Slc15a3</i>	Solute carrier family 15, member 3	NM_023044	0	0	0	0	0	6.74	2.34	2.88	3.49
<i>C1qg</i>	Complement component 1, q subcomponent, gamma	NM_007574	0	0	0	0	0	82.06	39.22	2.09	3.48
<i>Ly86</i>	Lymphocyte antigen 86	NM_010745	0	0	0	0	0	16.67	7.32	2.28	3.47
<i>AK029112</i>	Cybrd1 protein	AK029112	0	0	0	0	0	4.58	1.24	3.70	3.47
<i>Fit1</i>	Ferritin light chain 1	NM_010240	0	0	0	0	0	33.68	16.07	2.10	3.45
<i>AK141670</i>	Lysosomal acid lipase 1	AK141670	1	0	1	0	0	18.56	8.58	2.16	3.45
<i>Piscr2</i>	Phospholipid scramblase 2	NM_008880	0	0	0	0	0	3.30	0.75	4.41	3.44
<i>Ctss</i>	Cathepsin S	AK028366	0	0	0	0	0	107.38	52.02	2.06	3.42
<i>Lcn2</i>	Lipocalin 2	NM_008491	0	0	0	0	0	4.10	1.03	3.99	3.42
<i>Tlr2</i>	Toll-like receptor 2	NM_011905	0	0	0	0	0	5.61	1.75	3.21	3.40
<i>Unc93b1</i>	Unc93 homolog B	NM_019449	1	0	1	0	0	20.40	9.91	2.06	3.38
<i>Cd274</i>	CD274 antigen	NM_021893	0	0	0	0	0	4.75	1.37	3.47	3.38
<i>Cd9</i>	Cd9 antigen	NM_007657	0	0	0	0	0	44.66	21.83	2.05	3.33
<i>Apoc1</i>	Apolipoprotein C-I	NM_007469	0	0	0	0	0	3.18	0.74	4.29	3.32
<i>Hexa</i>	Hexosaminidase A	AK150901	3	0	3	0	0	34.64	16.94	2.04	3.32
<i>Igfbp5</i>	Insulin-like growth factor binding protein 5	NM_010518	0	0	0	0	0	128.27	63.50	2.02	3.32
<i>Anxa2</i>	Anxa2 protein	BC004659	0	0	0	0	0	7.60	2.86	2.65	3.29
<i>Glipr1</i>	GLI pathogenesis-related 1 (glioma)	NM_028608	0	0	0	0	0	3.45	0.84	4.09	3.29
<i>Pdpn</i>	Glycoprotein 38 precursor (GP38)	BC026551	0	0	0	0	0	15.04	6.93	2.17	3.29
<i>Psmb8</i>	Proteasome subunit beta type 8 precursor	BC013785	0	0	0	0	0	3.36	0.81	4.14	3.29
<i>Hspb6</i>	Heat shock protein, alpha-crystallin-related	NM_001012401	0	0	0	0	0	7.11	2.68	2.65	3.23
<i>5430435G22Rik</i>	Ras-related protein Rab-7b	AK030688	0	0	0	0	0	4.86	1.51	3.22	3.23
<i>Tmem10</i>	Transmembrane protein 10	NM_153520	1	0	1	0	0	14.00	6.33	2.21	3.23
<i>Trim25</i>	Tripartite motif protein 25	AK169562	0	0	0	0	0	6.39	2.35	2.72	3.22
<i>H2-T23</i>	Histocompatibility 2, T region locus 23	NM_010398	0	0	0	0	0	12.19	5.55	2.20	3.21
<i>Ms4a6c</i>	Ms4a6c protein	BC062247	0	0	0	0	0	2.10	0.52	4.08	3.20
<i>Axl</i>	AXL receptor tyrosine kinase	NM_009465	1	0	1	0	0	20.86	10.40	2.01	3.20
<i>H2-Q1</i>	MHC class I Q4 beta-2-microglobulin (Qb-1)	AK037574	0	0	0	0	0	7.52	2.85	2.64	3.19
<i>Tubb6</i>	Tubulin beta-5 chain (Beta-tubulin class-V) homolog	BC008225	0	0	0	0	0	2.19	0.54	4.03	3.16
<i>Tnfrsf1a</i>	Tumor necrosis factor receptor superfamily	NM_011609	0	0	0	0	0	10.35	4.37	2.37	3.15
<i>Lcp1</i>	Lymphocyte cytosolic protein 1	NM_008879	0	0	0	0	0	10.43	4.40	2.37	3.14
<i>Ggt1a1</i>	Glycoprotein galactosyltransferase alpha 1, 3	AK088605	0	0	0	0	0	8.84	3.48	2.54	3.14
<i>Lrrc47</i>	Leucine rich repeat containing 47	NM_201226	2	0	0	1	1	35.00	17.95	1.95	3.13
<i>Dhrs1</i>	Dehydrogenase/reductase (SDR family) member 1	NM_026819	0	0	0	0	0	42.45	21.35	1.99	3.13
<i>Cd22</i>	CD22 antigen	AK171589	0	0	0	0	0	4.48	1.36	3.29	3.12
<i>Arhgdib</i>	Rho, GDP dissociation inhibitor (GDI) beta	NM_007486	0	0	0	0	0	19.72	9.76	2.02	3.09
<i>Slc14a1</i>	Urea transporter, erythrocyte (Urea transporter B) (UT-B)	AK153891	0	0	0	0	0	12.80	6.01	2.13	3.09
<i>Trim21</i>	Tripartite motif protein 21	AK141294	0	0	0	0	0	3.70	1.03	3.59	3.08
<i>Nfe2l2</i>	Nuclear factor erythroid 2 related factor 2	U20532	0	0	0	0	0	17.09	8.45	2.02	3.08
<i>Fabp7</i>	Fatty acid binding protein 7, brain	NM_021272	0	0	0	0	0	10.95	4.83	2.27	3.08
<i>BC089618</i>	Novel protein similar to extracellular proteinase inhibitor Expi	BC089618	0	0	0	0	0	2.71	0.69	3.93	3.06
<i>Sfrp5</i>	Secreted frizzled-related sequence protein 5	NM_018780	0	0	0	0	0	3.18	0.83	3.81	3.05
<i>D12Ert647e</i>	Hypothetical protein LOC52668 isoform 2	NM_194066	0	0	0	0	0	16.90	8.51	1.99	3.04
<i>Capg</i>	Gelsolin-like capping protein	NM_007599	0	0	0	0	0	3.46	0.93	3.70	3.03
<i>Pik3ap1</i>	Phosphoinositide-3-kinase adaptor protein 1	NM_031376	0	0	0	0	0	5.62	1.99	2.83	3.03
<i>Tim1</i>	Metalloproteinase inhibitor 1 precursor	BC008107	0	0	0	0	0	1.86	0.50	3.70	3.01

<i>Cd63</i>	Cd63 antigen	NM_007653	0	0	0	0	0	26.25	14.29	1.84	2.99
1810029B16Rik	Hypothetical protein LOC66282	NM_025465	0	0	0	0	0	6.39	2.51	2.55	2.99
<i>Ctsc</i>	Cathepsin C preprotein	NM_009982	0	0	0	0	0	10.99	4.96	2.21	2.98
<i>Gusb</i>	Beta-glucuronidase structural	BC004616	0	0	0	0	0	11.23	5.15	2.18	2.98
<i>Stat2</i>	Stat2 protein	AF206162	0	0	0	0	0	14.11	6.79	2.08	2.97
<i>Parp12</i>	Poly (ADP-ribose) polymerase family, member 12	NM_172893	1	0	1	0	0	7.20	2.87	2.51	2.97
<i>Tcn2</i>	Transcobalamin 2	NM_015749	0	0	0	0	0	19.96	10.54	1.89	2.96
<i>Fcgr1</i>	Fc receptor, IgG, high affinity I	NM_010186	0	0	0	0	0	6.63	2.64	2.52	2.96
<i>Csf2rb2</i>	Colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-macrophage)	AK155626	0	0	0	0	0	2.04	0.55	3.70	2.95
<i>C5r1</i>	Complement component 5, receptor 1	NM_007577	0	0	0	0	0	3.23	0.88	3.67	2.95
<i>Cd151</i>	Cd151 protein	BC012236	0	0	0	0	0	13.80	6.75	2.05	2.93
<i>Cmtrn3</i>	CKLF-like MARVEL transmembrane domain-containing protein 3 (Chemokine-like factor superfamily member 3)	BC003230	0	0	0	0	0	7.46	3.07	2.43	2.92
<i>Epst1</i>	Epithelial stromal interaction 1 isoform b	NM_178825	0	0	0	0	0	1.90	0.52	3.62	2.91
<i>Bzrp</i>	Peripheral benzodiazepine receptor	NM_009775	0	0	0	0	0	4.33	1.42	3.06	2.88
0610039P13Rik	Hypothetical protein LOC74096	NM_028752	0	0	0	0	0	9.16	3.95	2.32	2.88
<i>Rpl39</i>	Ribosomal protein L39	NM_026055	0	0	0	0	0	11.50	5.32	2.16	2.87
<i>Scotin</i>	Scotin isoform 1	NM_025858	1	0	0	0	1	22.93	12.42	1.85	2.87
<i>Bcl3</i>	B-cell leukemia/lymphoma 3	NM_033601	0	0	0	0	0	2.60	0.71	3.68	2.85
<i>Cnn3</i>	Calponin 3, acidic	NM_028044	2	0	1	0	1	26.55	14.74	1.80	2.85
<i>Ifi47</i>	Interferon gamma inducible protein 47	NM_008330	0	0	0	0	0	1.77	0.52	3.40	2.83
<i>Adfp</i>	Adipose differentiation related protein	NM_007408	0	0	0	0	0	5.59	2.19	2.55	2.83
<i>Tnfrsf1b</i>	Tumor necrosis factor receptor superfamily,	NM_011610	0	0	0	0	0	7.31	3.11	2.35	2.83
<i>Lhfp12</i>	Lipoma HMGIC fusion partner-like 2	NM_172589	1	0	1	0	0	11.88	5.89	2.02	2.82
<i>Ifi35</i>	Interferon-induced protein 35	NM_027320	0	0	0	0	0	3.02	0.84	3.57	2.82
<i>Emp3</i>	Epithelial membrane protein 3	NM_010129	0	0	0	0	0	2.29	0.63	3.66	2.82
<i>Tcf7l2</i>	Transcription factor 7-like 2	AJ223070	9	0	9	0	0	5.23	1.95	2.69	2.82
AK128969	Hypothetical Peptidase family M20/M25/M40 containing protein	AK128969	0	0	0	0	0	4.50	1.50	3.00	2.81
<i>Tgm2</i>	Transglutaminase 2, C polypeptide	NM_009373	0	0	0	0	0	7.86	3.34	2.35	2.81
<i>Lgmn</i>	Legumain	NM_011175	4	0	4	0	0	49.09	27.55	1.78	2.81
<i>Ucp2</i>	Uncoupling protein 2	NM_011671	0	0	0	0	0	11.71	5.81	2.01	2.79
<i>Ela1</i>	Elastase 1, pancreatic	NM_033612	0	0	0	0	0	2.64	0.74	3.57	2.79
<i>D11Lgp2e</i>	DNA segment, Chr 11, Lothar Hennighausen 2,	NM_030150	0	0	0	0	0	2.49	0.69	3.61	2.76
<i>Cd74</i>	Ia-associated invariant chain	NM_010545	0	0	0	0	0	7.68	3.34	2.30	2.73
<i>Tgfbr2</i>	Transforming growth factor, beta receptor II	NM_009371	0	0	0	0	0	10.18	4.75	2.14	2.73
<i>Rac2</i>	RAS-related C3 botulinum substrate 2	NM_009008	0	0	0	0	0	4.47	1.58	2.83	2.72
<i>Apoe</i>	Apolipoprotein E	NM_009696	0	0	0	0	0	556.59	314.21	1.77	2.71
<i>Olig2</i>	Oligodendrocyte transcription factor 2	NM_016967	0	0	0	0	0	13.58	6.98	1.94	2.71
<i>Anxa3</i>	Annexin A3	AK169423	0	0	0	0	0	9.95	4.68	2.13	2.71
<i>Apod</i>	Apolipoprotein D	NM_007470	0	0	0	0	0	84.02	47.53	1.77	2.70
<i>Slc11a1</i>	Solute carrier family 11	NM_013612	0	0	0	0	0	6.06	2.55	2.38	2.70
<i>Cxcl16</i>	Chemokine (C-X-C motif) ligand 16	NM_023158	0	0	0	0	0	4.46	1.58	2.83	2.70
<i>Rab31</i>	Rab31 protein	BC013063	9	0	9	0	0	36.69	20.69	1.77	2.70
<i>Fcgr3</i>	Fcgr3 protein	BC052819	0	0	0	0	0	26.35	15.06	1.75	2.69
BC016112	Col20a1 protein	BC016112	0	0	0	0	0	2.62	0.76	3.43	2.68
<i>P2ry13</i>	Purinergic receptor P2Y13	NM_028808	0	0	0	0	0	11.97	6.17	1.94	2.68
<i>Ctsh</i>	Cathepsin H	NM_007801	1	0	1	0	0	13.22	6.76	1.96	2.67
1810009M01Rik	LR8 protein	NM_023056	0	0	0	0	0	23.57	13.38	1.76	2.66
<i>Mcam</i>	Cell surface glycoprotein MUC18 precursor	AB035509	0	0	0	0	0	9.44	4.35	2.17	2.66
<i>Rps27l</i>	Ribosomal protein S27-like	NM_026467	0	0	0	0	0	7.61	3.38	2.25	2.65
<i>Abhd4</i>	Abhydrolase domain containing 4	NM_134076	0	0	0	0	0	38.83	21.78	1.78	2.65
<i>Zfp36l1</i>	Zinc finger protein 36, C3H type-like 1	NM_007564	0	0	0	0	0	17.26	9.32	1.85	2.64
<i>Ctsl</i>	Cathepsin L precursor	AK159511	0	0	0	0	0	62.27	35.74	1.74	2.64
<i>Bcl2a1b</i>	B-cell leukemia/lymphoma 2 related protein A1b	NM_007534	0	0	0	0	0	2.30	0.67	3.44	2.63
<i>Ctsb</i>	Cathepsin B preproprotein	NM_007798	1	0	0	0	1	174.71	100.36	1.74	2.63
061001104Rik	Hepatocellular carcinoma-associated antigen 112	NM_025326	0	0	0	0	0	10.51	5.16	2.04	2.63
<i>Dbi</i>	Diazepam binding inhibitor isoform 1	NM_001037999	0	0	0	0	0	55.28	31.49	1.76	2.62
<i>Prg1</i>	Proteoglycan 1, secretory granule	NM_011157	0	0	0	0	0	8.49	3.85	2.20	2.61
<i>Icam1</i>	Intercellular adhesion molecule	NM_010493	0	0	0	0	0	4.49	1.70	2.65	2.60
<i>Cd109</i>	Hypothetical Alpha-macroglobulin receptor domain/Terpenoid cyclases/Protein prenyltransferases structure containing protein	BC052443	0	0	0	0	0	2.38	0.70	3.39	2.59
<i>Ccl3</i>	Chemokine (C-C motif) ligand 3	NM_011337	0	0	0	0	0	3.94	1.33	2.96	2.59
<i>Waspip</i>	Wiskott-Aldrich syndrome protein interacting	NM_153138	2	0	2	0	0	12.07	6.37	1.90	2.59
<i>Npc2</i>	Niemann Pick type C2	NM_023409	0	0	0	0	0	43.30	24.85	1.74	2.59
<i>Aqp4</i>	Aquaporin-4 (AQP-4) (WCH4) (Mercurial-insensitive water channel) (MIWC)	BC024526	1	0	1	0	0	35.71	20.55	1.74	2.59
<i>Rps14</i>	Ribosomal protein S14	NM_020600	1	0	1	0	0	21.63	12.39	1.75	2.57
<i>Parp3</i>	Poly (ADP-ribose) polymerase family, member 3	NM_145619	0	0	0	0	0	5.57	2.37	2.35	2.57
<i>Trim14</i>	Tripartite motif-containing 14	AK148837	0	0	0	0	0	2.07	0.64	3.23	2.57
<i>Tspan2</i>	Hypothetical CD9/CD37/CD63 antigens containing protein	AK020982	1	0	0	0	1	44.17	25.55	1.73	2.57
<i>Cyr61</i>	Cysteine rich protein 61	NM_010516	0	0	0	0	0	5.91	2.59	2.28	2.57
<i>Aebp1</i>	AEBP1 protein	BC082577	0	0	0	0	0	8.49	3.94	2.16	2.56
<i>Tnfaiap2</i>	Tumor necrosis factor, alpha-induced protein 2	AK154405	0	0	0	0	0	2.85	0.87	3.27	2.56
<i>Dnase1l1</i>	Deoxyribonuclease I-like 1 precursor	BC023246	0	0	0	0	0	1.97	0.62	3.19	2.56
<i>Tnc</i>	Tenascin C (Hexabrachion)	AK085667	0	0	0	0	0	2.68	0.82	3.28	2.55
<i>Anxa5</i>	Annexin A5	NM_009673	1	0	1	0	0	21.03	12.04	1.75	2.55
<i>Ephx1</i>	Ephx1 protein	BC057857	1	0	1	0	0	18.49	10.10	1.83	2.54
AK153119	Hypothetical protein	AK153119	0	0	0	0	0	2.37	0.71	3.33	2.54
<i>Tlr7</i>	Toll-like receptor 7 precursor	AK154906	0	0	0	0	0	6.81	3.09	2.20	2.53
<i>Mmp2</i>	Matrix metalloproteinase 2	NM_008610	0	0	0	0	0	2.85	0.88	3.24	2.53

<i>Psmb9</i>	Proteasome (prosome, macropain) subunit, beta	NM_013585	0	0	0	0	0	2.14	0.66	3.22	2.53
<i>Pqcl3</i>	Similar to mannose-P-dolichol utilization defect 1 protein homolog	AK138680	0	0	0	0	0	2.42	0.73	3.30	2.53
<i>Mgst1</i>	Microsomal glutathione S-transferase 1	NM_019946	0	0	0	0	0	10.11	4.95	2.04	2.52
<i>Ms4a6d</i>	MS4A6D protein	NM_026835	0	0	0	0	0	4.62	1.80	2.57	2.52
<i>Zc3hav1</i>	Hypothetical protein	AK143568	0	0	0	0	0	3.61	1.22	2.95	2.51
<i>Zfp488</i>	Zinc finger protein 488	NM_001013777	0	0	0	0	0	4.02	1.46	2.76	2.51
<i>Tmem86a</i>	Hypothetical protein LOC67893	NM_026436	0	0	0	0	0	10.94	5.60	1.95	2.50
<i>Maff</i>	V-maf musculoaponeurotic fibrosarcoma oncogene	NM_010755	0	0	0	0	0	1.67	0.56	2.96	2.50
<i>Hexb</i>	Hexosaminidase B	NM_010422	0	0	0	0	0	75.76	44.83	1.69	2.50
<i>1110007F12Rik</i>	Hypothetical protein LOC68487	NM_197986	0	0	0	0	0	1.49	0.53	2.81	2.48
<i>AK051656</i>	Protein KIAA1949 homolog	AK051656	0	0	0	0	0	7.93	3.68	2.16	2.48
<i>Rps26</i>	40S ribosomal protein S26	BC100456	0	0	0	0	0	27.29	16.03	1.70	2.48
<i>Plek</i>	Pleckstrin	NM_019549	0	0	0	0	0	29.57	17.32	1.71	2.48
<i>Prkcd</i>	Protein kinase C, delta	NM_011103	3	0	3	0	0	9.26	4.51	2.05	2.47
<i>AK048742</i>	Similar to Chromodomain-helicase-DNA-binding protein	AK048742	3	0	3	0	0	4.75	1.90	2.49	2.47
<i>Plip</i>	Transmembrane 4 superfamily member 11	NM_026385	0	0	0	0	0	32.01	18.77	1.71	2.47
<i>Ppgb</i>	Protective protein for beta-galactosidase	NM_001038492	0	0	0	0	0	43.83	26.11	1.68	2.46
<i>Mpzl1</i>	Myelin protein zero-like 1	AK090278	5	0	5	0	0	13.64	7.37	1.85	2.46
<i>Aldh1a1</i>	Aldehyde dehydrogenase family 1, subfamily A1	NM_013467	0	0	0	0	0	18.51	10.33	1.79	2.45
<i>Ninj1</i>	Ninjurin 1	NM_013610	0	0	0	0	0	8.57	4.14	2.07	2.44
<i>Nek6</i>	NIMA (never in mitosis gene a)-related expressed	NM_021606	0	0	0	0	0	10.89	5.66	1.92	2.43
<i>BC013712</i>	Hypothetical protein LOC230787	NM_001033308	0	0	0	0	0	2.82	0.90	3.12	2.43
<i>Olfm13</i>	Olfactomedin-like 3	NM_133859	0	0	0	0	0	15.03	8.31	1.81	2.43
<i>Aif3</i>	Activating transcription factor ATF3b	BC019946	0	0	0	0	0	2.40	0.76	3.18	2.43
<i>Arxa4</i>	Annexin A4	AK032703	0	0	0	0	0	4.72	1.92	2.46	2.42
<i>Tspan4</i>	Tetraspanin 4	NM_053082	0	0	0	0	0	5.11	2.16	2.37	2.42
<i>Rpl32</i>	Ribosomal protein L32	NM_172086	1	0	1	0	0	23.83	14.34	1.66	2.42
<i>Dbp</i>	D site albumin promoter binding protein	NM_016974	0	0	0	0	0	23.96	14.46	1.66	2.42
<i>Clic1</i>	Chloride intracellular channel 1	NM_033444	0	0	0	0	0	8.39	4.02	2.09	2.41
<i>Col5a3</i>	Adipocyte-specific protein 6	AB040491	0	0	0	0	0	1.45	0.53	2.74	2.41
<i>Vat1</i>	Vesicle amine transport protein 1 homolog	NM_012037	0	0	0	0	0	26.33	15.78	1.67	2.41
<i>Lyn</i>	Tyrosine-protein kinase Lyn (EC 2.7.1.112)	BC031547	0	0	0	0	0	6.83	3.17	2.15	2.39
<i>S100a1</i>	S100 calcium binding protein A1	NM_011309	0	0	0	0	0	40.59	24.20	1.68	2.39
<i>Plau</i>	Plasminogen activator, urokinase	NM_008873	0	0	0	0	0	4.84	2.04	2.37	2.38
<i>Prdx1</i>	Peroxiredoxin 1	NM_011034	1	0	1	0	0	40.08	23.94	1.67	2.38
<i>Csf1</i>	Colony stimulating factor 1	NM_007778	0	0	0	0	0	12.14	6.65	1.82	2.38
<i>Tlr3</i>	Toll-like receptor 3	NM_126166	0	0	0	0	0	11.10	5.84	1.90	2.36
<i>Gpr17</i>	G protein-coupled receptor 17	NM_001025381	0	0	0	0	0	24.29	14.61	1.66	2.36
<i>Itgb5</i>	Integrin beta-5 precursor	BC058246	1	0	1	0	0	21.94	13.15	1.67	2.35
<i>Klk6</i>	Protease, serine, 18	NM_011177	0	0	0	0	0	8.26	4.00	2.07	2.35
<i>Tfr</i>	Transferrin	NM_133977	1	0	1	0	0	135.42	82.88	1.63	2.34
<i>Ccrl2</i>	Lipopolsaccharide inducible C-C chemokine	NM_017466	0	0	0	0	0	1.39	0.52	2.67	2.34
<i>P4ha3</i>	P4ha3 protein	BC082538	0	0	0	0	0	4.46	1.83	2.44	2.33
<i>Apobec3</i>	Apolipoprotein B editing complex 3	AK153719	0	0	0	0	0	5.37	2.44	2.20	2.32
<i>Gns</i>	Glucosamine (N-acetyl)-6-sulfatase	NM_029364	0	0	0	0	0	45.72	28.30	1.62	2.32
<i>Tcrg1</i>	T-cell, immune regulator 1	NM_016921	0	0	0	0	0	8.29	4.07	2.04	2.31
<i>Parvg</i>	Parvin, gamma	NM_022321	1	0	1	0	0	5.93	2.79	2.13	2.31
<i>AK042457</i>	Flavin containing monooxygenase 1	AK042457	0	0	0	0	0	6.68	3.22	2.07	2.31
<i>Serinc5</i>	Serine incorporator 5	NM_172588	5	0	4	1	0	37.22	22.46	1.66	2.31
<i>Gje1</i>	Gap junction epsilon-1 protein (Connexin-29)	AK147913	2	0	2	0	0	96.07	59.23	1.62	2.31
<i>Lxn</i>	Latexin	NM_016753	0	0	0	0	0	20.88	12.57	1.66	2.31
<i>A930021H16Rik</i>	Weakly similar to MICAL-like 2	AK151086	0	0	0	0	0	1.97	0.67	2.93	2.30
<i>Scopel1</i>	Serine carboxypeptidase 1	AK153485	0	0	0	0	0	15.18	8.64	1.76	2.30
<i>Sox9</i>	SRY-box containing gene 9	NM_011448	1	0	0	0	1	20.07	12.18	1.65	2.30
<i>Nupr1</i>	P8 protein	NM_019738	0	0	0	0	0	8.30	4.12	2.01	2.30
<i>Pros1</i>	Protein S (alpha)	AK145501	0	0	0	0	0	11.06	5.90	1.87	2.30
<i>Sfpi1</i>	Transcription factor PU.1	L03215	0	0	0	0	0	5.42	2.49	2.18	2.29
<i>Cflar</i>	CASP8 and FADD-like apoptosis regulator isoform	NM_207653	1	0	0	0	1	13.76	7.83	1.76	2.29
<i>Il10rb</i>	Interleukin-10 receptor beta chain precursor	AK160991	0	0	0	0	0	7.84	3.84	2.04	2.28
<i>Nes</i>	Nes protein (Fragment)	AF076623	0	0	0	0	0	7.21	3.52	2.05	2.28
<i>S100a13</i>	S100 calcium binding protein A13	NM_009113	0	0	0	0	0	12.91	7.24	1.78	2.28
<i>Psme1</i>	Proteasome (prosome, macropain) 28 subunit	NM_011189	0	0	0	0	0	9.19	4.67	1.97	2.27
<i>Evi2b</i>	Ecotropic viral integration site 2b	NM_146023	0	0	0	0	0	14.44	8.24	1.75	2.27
<i>Naglu</i>	Alpha-N-acetylglucosaminidase	NM_013792	0	0	0	0	0	8.57	4.29	2.00	2.27
<i>Glipr2</i>	GLI pathogenesis-related 2	NM_027450	0	0	0	0	0	3.49	1.30	2.68	2.27
<i>Ptpn6</i>	Tyrosine-protein phosphatase non-receptor type 6	AK132509	0	0	0	0	0	5.80	2.76	2.10	2.26
<i>BC060276</i>	Filamin C (Gamma-filamin) (Filamin 2)	BC060276	0	0	0	0	0	2.56	0.87	2.94	2.26
<i>BC046309</i>	Novel protein	BC046309	0	0	0	0	0	4.31	1.78	2.42	2.26
<i>Sparc</i>	Secreted acidic cysteine rich glycoprotein	AK148670	3	0	1	0	2	119.54	74.49	1.60	2.26
<i>Apob4Br</i>	Apolipoprotein B48 receptor	NM_138310	0	0	0	0	0	1.61	0.59	2.70	2.25
<i>Cd300d</i>	MAIR-lib	AB091768	0	0	0	0	0	9.78	5.12	1.91	2.25
<i>Tgif</i>	TG-interacting factor	NM_009372	0	0	0	0	0	2.94	1.03	2.86	2.25
<i>Id3</i>	Inhibitor of DNA binding 3	NM_008321	0	0	0	0	0	16.04	9.47	1.69	2.25
<i>Litaf</i>	LPS-induced TN factor	NM_019980	1	0	1	0	0	18.08	10.54	1.72	2.24
<i>5830484A20Rik</i>	Hypothetical SAND/Sp100 containing protein	AK150373	0	0	0	0	0	1.42	0.55	2.58	2.24
<i>Hcls1</i>	Hematopoietic cell specific Lyn substrate 1	NM_008225	0	0	0	0	0	5.13	2.27	2.26	2.23
<i>Pabpc1</i>	Poly A binding protein, cytoplasmic 1	NM_008774	0	0	0	0	0	55.02	34.31	1.60	2.22
<i>Usp2</i>	Ubiquitin-specific protease 2 isoform Usp2-45	NM_198091	1	0	1	0	0	22.60	13.99	1.62	2.22

<i>Ptprc</i>	Protein tyrosine phosphatase, receptor type, C	NM_011210	2	0	1	0	1	4.38	1.86	2.36	2.21
<i>Sdc4</i>	Sdc4 protein	BC002312	3	0	0	0	3	46.40	29.47	1.57	2.21
<i>Clu</i>	Clusterin	NM_013492	1	0	0	0	1	259.47	163.59	1.59	2.20
<i>H2-Eb1</i>	Histocompatibility 2, class II antigen E beta	NM_010382	0	0	0	0	0	2.45	0.85	2.87	2.20
<i>Ikbke</i>	Inhibitor of kappaB kinase epsilon	NM_019777	0	0	0	0	0	1.67	0.62	2.70	2.20
<i>Slc7a2</i>	Solute carrier family 7 (cationic amino acid)	NM_007514	4	0	0	0	4	18.08	10.65	1.70	2.20
<i>Lamp2</i>	Lysosomal membrane glycoprotein 2 isoform 1	NM_001017959	0	0	0	0	0	29.58	18.32	1.61	2.20
<i>H2-Aa</i>	Histocompatibility 2, class II antigen A, alpha	NM_010378	0	0	0	0	0	3.69	1.40	2.64	2.20
<i>Tor3a</i>	Torsin family 3, member A	BC071216	0	0	0	0	0	5.58	2.69	2.08	2.19
<i>Arf11</i>	ADP-ribosylation factor-like 11	NM_177337	0	0	0	0	0	2.92	1.05	2.80	2.19
<i>Hspb8</i>	Heat shock protein 20-like protein	NM_030704	0	0	0	0	0	10.56	5.80	1.82	2.19
<i>Stat5a</i>	Signal transducer and activator of transcription	NM_011488	0	0	0	0	0	1.38	0.54	2.54	2.19
<i>Rnf122</i>	Hypothetical RING finger containing protein	AK171823	0	0	0	0	0	5.33	2.52	2.12	2.19
<i>Tgfb1</i>	Transforming growth factor-beta-induced protein Ig-h3 precursor (Beta Ig-h3)	AK155828	0	0	0	0	0	3.85	1.52	2.54	2.19
<i>Fgl2</i>	Fibrinogen-like protein 2	NM_008013	0	0	0	0	0	2.20	0.76	2.88	2.18
<i>Erbb2ip</i>	Erbb2 interacting protein isoform 2	NM_021563	15	0	14	1	0	52.87	33.12	1.60	2.18
<i>Slc6a6</i>	Solute carrier family 6 (neurotransmitter transporter, taurine), member 6	AK162776	10	0	7	0	3	65.13	41.37	1.57	2.17
<i>Ptgds2</i>	Prostaglandin D2 synthase 2, hematopoietic	NM_019455	0	0	0	0	0	8.10	4.14	1.95	2.17
<i>Rgma</i>	RGM domain family, member A	NM_177740	0	0	0	0	0	21.16	13.15	1.61	2.17
<i>Ehd4</i>	EH domain containing protein MPAST2	NM_133838	0	0	0	0	0	8.51	4.41	1.93	2.16
<i>Lats2</i>	LATS2B	AY015061	3	0	2	0	1	8.99	4.72	1.90	2.16
<i>Add3</i>	Adducin 3 (gamma)	AK144174	14	0	14	0	0	38.18	23.73	1.61	2.15
<i>Csf2rb1</i>	Colony stimulating factor 2 receptor, beta 1, low-affinity (granulocyte-macrophage)	AK170199	0	0	0	0	0	2.66	0.94	2.84	2.15
9230117N10Rik	Interleukin 33	NM_133775	0	0	0	0	0	35.00	22.20	1.58	2.14
<i>AK046834</i>	Hypothetical ATP-dependent DNA ligase containing protein	AK046834	1	0	1	0	0	6.80	3.39	2.01	2.14
<i>Ctdsp1</i>	CTD (carboxy-terminal domain, RNA polymerase II	NM_153088	0	0	0	0	0	18.40	11.18	1.65	2.13
<i>BC023356</i>	Transcription factor SOX-10 (SOX-21) (Transcription factor SOX-M)	BC023356	0	0	0	0	0	19.60	12.35	1.59	2.10
<i>Gm2a</i>	GM2 ganglioside activator protein	NM_010299	0	0	0	0	0	44.63	28.75	1.55	2.10
<i>Rhoc</i>	Ras homolog gene family, member C	NM_007484	0	0	0	0	0	8.55	4.50	1.90	2.10
<i>Chi3l1</i>	Chitinase 3-like 1	NM_007695	0	0	0	0	0	7.43	3.80	1.95	2.10
<i>Vcam1</i>	Vascular cell adhesion molecule 1	AK030195	0	0	0	0	0	12.23	7.14	1.71	2.10
<i>Rpl14</i>	Ribosomal protein L14	NM_025974	0	0	0	0	0	13.16	7.69	1.71	2.09
<i>Arpep</i>	Alanyl (membrane) aminopeptidase	NM_008486	1	0	1	0	0	3.27	1.25	2.63	2.09
<i>Ly6e</i>	Lymphocyte antigen Ly-6E precursor	BC005684	0	0	0	0	0	66.62	43.05	1.55	2.09
<i>Pbxip1</i>	Pre-B-cell leukemia transcription factor	NM_146131	0	0	0	0	0	19.28	12.04	1.60	2.09
<i>Cldn11</i>	Claudin 11	NM_008770	1	0	1	0	0	121.77	78.83	1.54	2.08
<i>Cpne3</i>	Copine III	NM_027769	4	0	3	0	1	12.09	7.11	1.70	2.07
<i>Sema6a</i>	Sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	AK042751	4	0	4	0	0	10.85	6.10	1.78	2.07
<i>Hps6</i>	Heparanase	NM_152803	0	0	0	0	0	2.46	0.91	2.72	2.07
<i>Il1a</i>	Interleukin 1 alpha	NM_010554	0	0	0	0	0	2.04	0.76	2.69	2.06
<i>Ltbr</i>	Lymphotxin B receptor	NM_010736	0	0	0	0	0	5.40	2.68	2.01	2.05
<i>S100a4</i>	S100 calcium binding protein A4	NM_011311	0	0	0	0	0	3.08	1.19	2.60	2.05
<i>Syng2</i>	Synaptogyrin 2	NM_009304	0	0	0	0	0	6.68	3.44	1.94	2.05
<i>Cd83</i>	CD83 antigen	BC107344	0	0	0	0	0	8.06	4.24	1.90	2.05
<i>Pycard</i>	PYD and CARD domain containing	NM_023258	0	0	0	0	0	3.35	1.35	2.48	2.04
<i>Dap</i>	Death-associated protein	NM_146057	0	0	0	0	0	5.44	2.73	1.99	2.04
<i>Trp53inp1</i>	Transformation related protein 53 inducible	NM_021897	0	0	0	0	0	9.11	4.94	1.84	2.04
<i>Cotl1</i>	Coactosin-like protein	BC010249	3	0	3	0	0	42.36	27.47	1.54	2.04
<i>Stom</i>	Stom protein	BC003789	0	0	0	0	0	9.75	5.41	1.80	2.04
<i>Pdim4</i>	Reversion induced LIM gene	NM_019417	0	0	0	0	0	5.47	2.73	2.00	2.04
<i>Npl</i>	N-acetylneuraminate pyruvate lyase	NM_028749	0	0	0	0	0	5.27	2.60	2.03	2.04
<i>Sapl1</i>	Sphingosine phosphate lyase 1	NM_009163	1	0	1	0	0	22.27	14.29	1.56	2.04
<i>Cacng5</i>	Voltage-dependent calcium channel gamma-5	NM_080644	3	0	3	0	0	7.26	3.80	1.91	2.03
4930429M06Rik	Hypothetical Actin-crosslinking proteins containing protein	AK090002	1	0	1	0	0	4.32	1.94	2.22	2.03
<i>Tal1</i>	T-cell acute lymphocytic leukemia 1	NM_011527	0	0	0	0	0	1.36	0.57	2.39	2.02
<i>Necap2</i>	Adaptin-ear-binding coat-associated protein 2	NM_025383	1	0	1	0	0	18.09	11.08	1.63	2.02
<i>Bag3</i>	Bcl2-associated athanogene 3	NM_013863	0	0	0	0	0	6.88	3.62	1.90	2.02
<i>Man2b2</i>	Mannosidase alpha class 2B member 2	NM_008550	1	0	1	0	0	16.04	9.90	1.62	2.01
<i>Vamp8</i>	Vesicle-associated membrane protein 8	NM_016794	0	0	0	0	0	9.46	5.26	1.80	2.01
<i>Irf8</i>	Interferon consensus sequence binding protein 1	BC005450	1	0	1	0	0	5.86	3.00	1.95	2.01
<i>Stat3</i>	Signal transducer and activator of transcription	NM_011486	3	0	3	0	0	20.13	12.93	1.56	2.01
<i>D3Ucla1</i>	Stress-associated endoplasmic reticulum protein	NM_030685	1	0	0	0	1	29.42	18.99	1.55	2.01
<i>Ccng1</i>	Cyclin G1	NM_009831	0	0	0	0	0	35.70	23.34	1.53	2.00
<i>Loh11cr2a</i>	Loss of heterozygosity, 11, chromosomal region	NM_172767	1	0	0	0	1	11.14	6.60	1.69	2.00

Supplementary Table 2 Genes downregulated upon TDP-43 depletion in adult mouse brain

Gene symbol	Protein	Refseq/mRNA identifier	CLIP-seq number of clusters					RNA-seq			
			Total	in 5'UTR	in introns	in exons	in 3'UTR	RPKM in TDP-43 KD	RPKM in control	Ratio KD/control	
<i>Tcb1</i>	T-cell lymphoma breakpoint associated target 1	NM_001025286	58	0	57	1	0	3.16	18.06	0.18	-8.17
<i>Tardbp</i>	TAR DNA binding protein isoform 5	NM_001003898	5	0	0	0	5	10.17	43.61	0.23	-6.91
<i>Cadps</i>	Calcium-dependent secretion activator 1	BC079679	56	0	56	0	0	7.62	23.80	0.32	-5.90
<i>Csmd1</i>	CUB and Sushi multiple domains 1	NM_053171	154	0	152	1	1	2.51	9.43	0.27	-5.39
<i>Ctnna2</i>	Ctnna2 protein	BC079648	115	0	115	0	0	8.80	22.44	0.39	-4.88
<i>Car10</i>	Hypothetical carbonic anhydrase structure containing protein	AK012302	52	1	51	0	0	6.05	15.81	0.38	-4.67
<i>C1stn2</i>	Calsyntenin 2	NM_022319	38	0	38	0	0	7.70	19.32	0.40	-4.59
<i>Nrg3</i>	Neuregulin 3	NM_008734	132	0	131	0	1	2.75	8.15	0.34	-4.47
2900006F19Rik	Hypothetical protein LOC72899	NM_028387	36	0	36	0	0	2.94	8.52	0.34	-4.35
<i>Adcy2</i>	Adenylate cyclase 2	NM_153534	15	0	15	0	0	8.57	20.60	0.42	-4.25
<i>Kcnd2</i>	Potassium voltage-gated channel, Shal-related	NM_019697	78	0	77	0	1	14.60	34.39	0.42	-4.18
<i>Lrp1b</i>	Low density lipoprotein-related protein 1B (deleted in tumors)	AK136118	87	0	87	0	0	2.59	6.87	0.38	-4.08
<i>Cacna2d3</i>	Calcium channel, voltage-dependent, alpha2/delta	NM_009785	63	0	63	0	0	12.00	25.88	0.46	-4.05
<i>Nrxn3</i>	Neurexin III	BC060719	178	0	178	0	0	16.25	37.23	0.44	-3.93
<i>Hapln4</i>	Hyaluronan and proteoglycan link protein 4 precursor	AK034300	0	0	0	0	0	9.71	20.10	0.48	-3.86
<i>Kl</i>	Klotho	NM_013823	0	0	0	0	0	2.53	6.33	0.40	-3.84
<i>Park2</i>	Parkin	AF250294	39	0	39	0	0	0.63	2.18	0.29	-3.78
<i>Fgf14</i>	Fibroblast growth factor 14 isoform b	NM_207667	85	0	85	0	0	6.99	14.99	0.47	-3.76
<i>Sdk1</i>	Sidekick homolog 1	NM_177879	29	0	29	0	0	0.51	1.54	0.33	-3.69
<i>Efna5</i>	Ephrin A5 isoform 2	NM_010109	21	0	21	0	0	3.90	9.33	0.42	-3.69
<i>Kcnip4</i>	Kv channel interacting protein 4	AK148685	109	0	109	0	0	3.98	9.30	0.43	-3.58
<i>Cntnap2</i>	Contactin associated protein-like 2 isoform b	NM_025771	116	0	116	0	0	11.00	21.03	0.52	-3.52
<i>Tmem28</i>	Transmembrane protein 28	NM_173446	79	0	79	0	0	6.21	12.27	0.51	-3.49
<i>Sntg1</i>	Syntrophin, gamma 1	NM_027671	23	0	23	0	0	2.01	4.88	0.41	-3.43
<i>Hs6st3</i>	Heparan sulfate 6-O-sulfotransferase 3	NM_015820	80	0	79	0	1	4.14	8.95	0.46	-3.35
AK134882	Hypothetical protein	AK134882	2	0	2	0	0	2.47	5.55	0.44	-3.33
<i>Kcnj3</i>	Potassium inwardly-rectifying channel J3	NM_008426	21	0	21	0	0	6.57	12.70	0.52	-3.32
<i>Hdh</i>	Huntington disease gene homolog	NM_010414	10	0	9	1	0	8.52	16.55	0.51	-3.29
<i>Arc</i>	Activity regulated cytoskeletal-associated	NM_018790	0	0	0	0	0	25.40	50.51	0.50	-3.29
<i>Rims1</i>	Rims1 protein	BC055294	6	0	6	0	0	15.32	29.50	0.52	-3.25
<i>Klf10</i>	Kruppel-like factor 10	NM_013692	0	0	0	0	0	6.55	12.13	0.54	-3.19
<i>Nlgn1</i>	Neuroligin 1	NM_138666	102	0	101	1	0	8.55	16.28	0.53	-3.19
<i>Kcnk4</i>	TRAAK	NM_008431	0	0	0	0	0	0.76	2.07	0.37	-3.16
<i>Folr1</i>	Folate receptor 1	NM_008034	0	0	0	0	0	0.67	1.81	0.37	-3.16
<i>Slc17a8</i>	Vesicular glutamate transporter-3	NM_182959	0	0	0	0	0	1.08	2.84	0.38	-3.16
<i>Kcnh7</i>	Similar to potassium channel protein erg long isoform	AK034003	23	0	23	0	0	2.90	5.92	0.49	-3.12
AK171114	weakly similar to Keratin 8	AK171114	0	0	0	0	0	0.56	1.39	0.40	-3.11
<i>Chat</i>	Choline acetyltransferase	NM_009891	2	0	2	0	0	0.97	2.59	0.37	-3.11
<i>Rgs6</i>	Regulator of G-protein signaling 6	NM_015812	37	0	37	0	0	1.68	4.03	0.42	-3.10
<i>Slt3</i>	Slit homolog 3	NM_011412	40	0	40	0	0	4.10	8.39	0.49	-3.10
<i>Grm7</i>	Glutamate receptor, metabotropic 7	NM_177328	78	0	77	1	0	8.82	16.33	0.54	-3.09
<i>Ptpn2</i>	Protein tyrosine phosphatase, receptor type, N polypeptide 2	AK138655	64	0	63	0	1	18.06	34.41	0.52	-3.08
<i>Lsamp</i>	Limbic system-associated membrane protein	AK140043	71	0	70	0	1	15.54	28.93	0.54	-3.07
<i>Opcml</i>	Opioid binding protein/cell adhesion	NM_177906	116	0	115	0	1	18.55	35.28	0.53	-3.06
4930431L04Rik	Hypothetical Glycosyl transferase, family 2 containing protein	BC11102	23	0	23	0	0	0.63	1.54	0.41	-3.00
<i>Ica1</i>	Islet cell autoantigen 1	NM_010492	16	0	16	0	0	4.83	9.23	0.52	-2.99
<i>Col8a2</i>	Procollagen, type VIII, alpha 2	NM_199473	0	0	0	0	0	0.61	1.46	0.42	-2.98
<i>Kcnq5</i>	KCNQ5 potassium channel	AK147264	36	0	36	0	0	14.96	26.18	0.57	-2.97
<i>Mapk11</i>	Mitogen-activated protein kinase 11	NM_011161	0	0	0	0	0	5.36	9.86	0.54	-2.97
<i>Gpc5</i>	Similar to BA93M14.1 (Glycanic 5)	AK084223	24	0	24	0	0	3.87	7.69	0.50	-2.96
<i>Sgc2</i>	Zeta-sarcoglycan (Zeta-SG) (ZSG1)	AK136779	56	1	55	0	0	0.74	1.85	0.40	-2.95
<i>Astr2</i>	Astroactin 2 isoform a	NM_019514	72	0	72	0	0	5.08	9.45	0.54	-2.95
<i>Otud7</i>	Hypothetical protein LOC170711	NM_130880	30	0	30	0	0	4.47	8.80	0.51	-2.95
<i>Kcnj6</i>	Potassium inwardly-rectifying channel, subfamily J, member 6	AK044218	28	0	27	0	1	3.28	6.37	0.52	-2.92
<i>Myl4</i>	Myosin, light polypeptide 4	NM_010858	0	0	0	0	0	2.83	5.55	0.51	-2.91
<i>Sostdc1</i>	Cystine knot-containing secreted protein	NM_025312	0	0	0	0	0	0.75	1.82	0.41	-2.90
<i>Npr3</i>	Natriuretic peptide receptor 3 isoform b	NM_001039181	2	0	2	0	0	0.64	1.52	0.43	-2.89
AK138471	Carboxyl-terminal PDZ ligand of neuronal nitric oxide synthase homolog	AK138471	38	0	38	0	0	5.60	9.97	0.56	-2.88
<i>Kirrel2</i>	Kin of IRRE-like 2	NM_172898	0	0	0	0	0	0.86	2.12	0.41	-2.85
<i>Vamp1</i>	Vesicle-associated membrane protein 1	BC049902	1	1	0	0	1	19.15	34.73	0.55	-2.83
<i>Trhde</i>	Thyrotropin-releasing hormone degrading	NM_146241	17	0	17	0	0	2.82	5.43	0.52	-2.81
<i>Gfra2</i>	Glial cell line derived neurotrophic factor	NM_008115	6	0	6	0	0	9.38	16.06	0.58	-2.80
C630028F04Rik	Hypothetical protein LOC243274	NM_172885	43	0	43	0	0	3.15	5.93	0.53	-2.79
<i>Adra1d</i>	Adrenergic receptor, alpha 1d	NM_013460	0	0	0	0	0	0.99	2.30	0.43	-2.77
<i>Upp2</i>	Weakly similar to uridine phosphorylase	BC027189	23	0	23	0	0	0.77	1.77	0.43	-2.76
C630007B19Rik	TAFA1 protein	NM_182808	56	0	56	0	0	1.93	4.10	0.47	-2.76
<i>Nrxn1</i>	Neurexin-1-alpha precursor (Neurexin I-alpha)	AB093249	162	0	162	0	0	18.66	33.28	0.56	-2.76
AB125594	Hypothetical Proline-rich region profile/Serine-rich region profile containing protein	AB125594	45	0	43	0	2	9.06	15.71	0.58	-2.76

Ptptr	Protein tyrosine phosphatase, receptor type, T	NM_021464	74	0	74	0	0	8.13	14.29	0.57	-2.75
<i>Grm8</i>	Glutamate receptor, metabotropic 8	NM_008174	21	0	21	0	0	1.18	2.67	0.44	-2.75
<i>Siglech</i>	SIGLEC-like protein	NM_178706	0	0	0	0	0	6.14	10.50	0.59	-2.74
<i>Ryr2</i>	Ryr2 protein	BC043140	41	0	41	0	0	1.82	3.83	0.47	-2.73
<i>Nrn1</i>	Neuritin 1	NM_153529	2	0	2	0	0	17.81	31.03	0.57	-2.73
<i>A830018L16Rik</i>	VEST-1 protein homolog	AK135047	8	0	8	0	0	15.04	24.75	0.61	-2.73
<i>Smyd3</i>	SET and MYND domain containing 3	NM_027188	39	0	39	0	0	4.41	8.20	0.54	-2.72
<i>Tssc1</i>	Tumor suppressing subtransferable candidate 1	NM_201357	6	0	6	0	0	4.51	8.29	0.54	-2.72
<i>AK161480</i>	Hypothetical protein	AK161480	0	0	0	0	0	0.55	1.18	0.46	-2.71
<i>Trpc3</i>	Transient receptor potential cation channel	NM_019510	3	0	3	0	0	3.69	6.83	0.54	-2.71
<i>Gabra3</i>	Gamma-aminobutyric acid (GABA-A) receptor	NM_008067	2	0	2	0	0	15.39	25.51	0.60	-2.71
<i>Aqp1</i>	Aquaporin 1	NM_007472	0	0	0	0	0	0.67	1.44	0.46	-2.68
<i>Plcb1</i>	Plcb1 protein	BC058710	59	0	59	0	0	24.54	44.03	0.56	-2.68
<i>Kcnk4</i>	Potassium channel subfamily K member 4	BC061075	0	0	0	0	0	0.57	1.21	0.47	-2.67
<i>Kcnma1</i>	Calcium-activated potassium channel alpha subunit 1	U09383	96	0	96	0	0	8.34	14.36	0.58	-2.66
<i>Cacna1c</i>	Calcium channel, voltage-dependent, L type,	NM_009781	77	0	77	0	0	5.57	9.56	0.58	-2.65
<i>Slc10a4</i>	Solute carrier family 10	NM_173403	0	0	0	0	0	1.24	2.70	0.46	-2.65
<i>E030025D05Rik</i>	E030025D05Rik protein	AK173298	20	1	18	0	1	6.06	10.10	0.60	-2.62
<i>Ttr</i>	Transthyretin	NM_013697	0	0	0	0	0	44.88	80.56	0.56	-2.62
<i>Slc30a3</i>	Zinc transporter 3 (ZnT-3) (Solute carrier family 30 member 3)	BC066199	0	0	0	0	0	5.66	9.55	0.59	-2.60
<i>Kcn3</i>	Potassium voltage-gated channel,	NM_173417	0	0	0	0	0	0.58	1.20	0.48	-2.60
<i>493343F18Rik</i>	Hypothetical protein LOC66771	NM_025757	1	1	0	0	0	29.33	51.30	0.57	-2.59
<i>Satb2</i>	Two cut domains-containing homeodomain protein	NM_139146	5	0	5	0	0	6.79	10.98	0.62	-2.58
<i>Kirrel3</i>	Kin of IRRE-like protein 3 precursor (Kin of irregular chiasm-like protein 3)	AK045373	74	0	74	0	0	6.02	9.99	0.60	-2.58
<i>F5</i>	Coagulation factor V	NM_007976	0	0	0	0	0	0.94	2.08	0.45	-2.57
<i>2810401C16Rik</i>	Similar to neurula-specific ferodoxin reductase-like protein homolog	AK158809	3	0	2	0	1	10.73	17.93	0.60	-2.57
<i>Adcy1</i>	Adenylate cyclase 1	NM_009622	17	0	12	0	5	38.58	68.45	0.56	-2.56
<i>A130090K04Rik</i>	Hypothetical protein LOC320495	NM_001033391	3	0	3	0	0	2.68	4.95	0.54	-2.56
<i>Grin2a</i>	Glutamate receptor, ionotropic, NMDA2A (epsilon)	NM_008170	83	0	83	0	0	2.19	4.23	0.52	-2.56
<i>Cacna1e</i>	Calcium channel, voltage-dependent, R type	NM_009782	40	0	34	6	0	8.43	14.18	0.59	-2.55
<i>Fgf12</i>	Fibroblast growth factor 12 isoform b	NM_010199	81	0	81	0	0	16.54	27.53	0.60	-2.54
<i>Cpne4</i>	Weakly similar to copine VII	AK014396	8	0	8	0	0	7.73	12.71	0.61	-2.53
<i>0710005M24Rik</i>	Weakly similar to heterogeneous nuclear ribonucleoproteins C1/C2 (hnRNPC1/C2)	BC052358	59	1	57	0	1	7.07	11.27	0.63	-2.53
<i>Col19a1</i>	Procollagen, type XIX, alpha 1	NM_007733	3	0	3	0	0	0.61	1.24	0.49	-2.53
<i>AK018073</i>	Hypothetical calcium-binding EGF-like domain containing protein homolog	AK018073	39	0	39	0	0	0.57	1.16	0.49	-2.52
<i>Gpr26</i>	G protein-coupled receptor 26	NM_173410	2	0	2	0	0	10.21	16.56	0.62	-2.51
<i>Cpne9</i>	Similar to copine-like protein KIAA1599	AK044080	3	0	3	0	0	5.59	9.29	0.60	-2.51
<i>Dgkb</i>	Hypothetical EF-hand/Phorbol esters/diacylglycerol binding domain/Cytochrome c family heme-binding site containing protein	AK083222	28	0	28	0	0	35.79	62.69	0.57	-2.51
<i>BC030317</i>	Leucine-rich repeat-containing protein 17 precursor	BC030317	0	0	0	0	0	0.52	1.06	0.50	-2.50
<i>Camk4</i>	Calcium/calmodulin-dependent protein kinase IV	NM_009793	28	0	28	0	0	20.31	34.26	0.59	-2.48
<i>Odz1</i>	Odd Oz/ten-m homolog 1	NM_011855	26	0	26	0	0	2.37	4.38	0.54	-2.48
<i>Wwox</i>	WW-domain oxidoreductase	NM_019573	62	0	62	0	0	1.14	2.38	0.48	-2.47
<i>Igsf4d</i>	Weakly similar to BK134P22.1	AK046800	110	0	109	1	0	18.54	30.84	0.60	-2.47
<i>AK138164</i>	NB-2 homolog	AK138164	34	0	34	0	0	2.34	4.32	0.54	-2.47
<i>Grik2</i>	Glutamate receptor, ionotropic, kainate 2 (beta)	NM_010349	52	0	52	0	0	17.00	27.85	0.61	-2.46
<i>Gfod1</i>	Hypothetical protein LOC328232	NM_001033399	20	0	20	0	0	15.37	23.88	0.64	-2.46
<i>Grin2c</i>	Glutamate receptor, ionotropic, NMDA2C (epsilon)	NM_010350	3	0	3	0	0	7.38	11.76	0.63	-2.45
<i>Klc2</i>	Klc2 protein	BC014845	0	0	0	0	0	15.86	24.95	0.64	-2.45
<i>Ttc15</i>	Weakly similar to CGI-87 PROTEIN	AK031763	2	0	2	0	0	10.60	16.93	0.63	-2.45
<i>L42339</i>	Sodium channel 3	L42339	2	0	2	0	0	8.94	14.67	0.61	-2.42
<i>Rtn4r</i>	Nogo receptor	NM_022982	4	0	4	0	0	7.34	11.59	0.63	-2.41
<i>Syt13</i>	Synaptotagmin XIII	NM_030725	4	0	3	0	1	18.66	30.56	0.61	-2.41
<i>Pdzd10</i>	Weakly similar to Hypothetical band 4.1 family containing protein	AK147370	63	0	63	0	0	9.67	15.47	0.62	-2.41
<i>Ecel1</i>	Damage-induced neuronal endopeptidase	NM_021306	0	0	0	0	0	2.49	4.46	0.56	-2.40
<i>Dpp10</i>	Dipeptidyl peptidase 10	NM_199021	75	0	74	0	1	10.39	16.43	0.63	-2.40
<i>Fbxw8</i>	F-box protein FBX29	AK015338	0	0	0	0	0	1.45	2.83	0.51	-2.39
<i>Ccbe1</i>	Collagen and calcium binding EGF domains 1	NM_178793	4	0	3	0	1	0.61	1.18	0.52	-2.37
<i>Slc24a3</i>	Solute carrier family 24	NM_053195	17	0	17	0	0	13.17	20.23	0.65	-2.36
<i>Snrp70</i>	U1 small nuclear ribonucleoprotein 70 kDa	NM_009224	2	0	1	1	0	69.49	117.85	0.59	-2.36
<i>Podxl2</i>	Podocalyxin-like 2	NM_176973	1	0	1	0	0	12.22	18.69	0.65	-2.35
<i>A930001M12Rik</i>	Hypothetical protein LOC320500	NM_177175	0	0	0	0	0	0.85	1.68	0.51	-2.34
<i>Gpr158</i>	G protein-coupled receptor 158 isoform b	NM_175706	20	0	20	0	0	29.70	48.92	0.61	-2.34
<i>Zfp180</i>	Zfp180 protein	BC063741	3	1	2	0	0	16.63	26.55	0.63	-2.34
<i>Cbln2</i>	Cerebellin 2 precursor protein	NM_172633	0	0	0	0	0	3.66	6.17	0.59	-2.33
<i>Stx1a</i>	Syntaxin 1A	NM_016801	1	0	1	0	0	24.86	41.33	0.60	-2.33
<i>Ncam2</i>	Neural cell adhesion molecule 2 precursor (N-CAM 2) (RB-8 neural cell adhesion molecule)	AF001287	37	0	37	0	0	7.79	12.23	0.64	-2.33
<i>Fosl2</i>	Fos-like antigen 2	AK145822	1	0	1	0	0	6.83	10.53	0.65	-2.32

<i>Pcdh7</i>	Protocadherin 7	NM_018764	0	0	0	0	0	8.97	14.37	0.62	-2.32
<i>Pde1a</i>	Phosphodiesterase 1A, calmodulin-dependent	NM_001009978	28	0	28	0	0	11.79	17.86	0.66	-2.32
<i>Tnfrsf25</i>	Tnfrsf25 protein	BC017526	1	0	1	0	0	1.64	3.11	0.53	-2.32
<i>Apba2bp</i>	Amyloid beta A4 protein-binding family A member 2-binding protein (X11L-binding protein 51) (mXB51)	AK013520	0	0	0	0	0	6.64	10.29	0.65	-2.31
<i>KcnS2</i>	K+ voltage-gated channel, subfamily S, 2	NM_181317	0	0	0	0	0	6.22	9.68	0.64	-2.30
<i>BC052055</i>	Hypothetical protein LOC328643	NM_182636	0	0	0	0	0	4.33	7.20	0.60	-2.30
<i>Alas2</i>	Aminolevulinic acid synthase 2, erythroid	NM_009653	0	0	0	0	0	0.53	1.00	0.53	-2.30
<i>D14Ertd171e</i>	CAZ-associated structural protein	NM_177814	62	0	61	0	1	17.51	27.80	0.63	-2.30
<i>Magi2</i>	Activin receptor interacting protein 1	AK147530	62	0	62	0	0	15.73	23.87	0.66	-2.30
<i>Galnt9</i>	UDP-N-acetyl-alpha-D-galactosamine:polypeptide	NM_198306	9	0	9	0	0	5.48	8.80	0.62	-2.30
<i>Nr4a3</i>	Orphan nuclear receptor NR4A3 (Orphan nuclear receptor TEC) (Translocated in extraskelatal chondrosarcoma)	BC068150	0	0	0	0	0	4.32	7.17	0.60	-2.30
<i>Cntn4</i>	Contactin 4	AK163520	37	0	37	0	0	6.24	9.63	0.65	-2.29
<i>Atp2b3</i>	Plasma membrane calcium ATPase 3	NM_177236	2	0	2	0	0	15.15	23.00	0.66	-2.28
<i>Kcnj9</i>	G protein-activated inward rectifier potassium channel 3 (GIRK3) (Potassium channel, inwardly rectifying subfamily J member 9) (Inwardly rectifier K(+) channel Kir3.3)	BC065161	0	0	0	0	0	14.13	21.28	0.66	-2.28
<i>Large</i>	like-glycosyltransferase	NM_010687	38	0	38	0	0	17.42	27.47	0.63	-2.28
<i>Accn1</i>	Accn1 protein	BC038551	110	0	110	0	0	5.29	8.55	0.62	-2.28
<i>Rasgrf2</i>	RAS protein-specific guanine nucleotide-releasing factor 2	AK158472	1	0	1	0	0	5.30	8.57	0.62	-2.27
<i>Xkr4</i>	XK-related protein 4	NM_001011874	42	0	42	0	0	3.75	6.24	0.60	-2.27
<i>Cabp1</i>	calcium binding protein 1	NM_013879	2	0	2	0	0	11.29	17.56	0.64	-2.26
<i>Scube1</i>	Scube1 protein	BC066066	4	0	4	0	0	3.63	5.88	0.62	-2.26
<i>Ephb6</i>	Eph receptor B6	NM_007680	1	0	1	0	0	13.80	20.81	0.66	-2.26
<i>AK147314</i>	Delta kalirin-7 homolog	AK147314	33	0	33	0	0	38.00	63.06	0.60	-2.25
<i>Wnt9a</i>	Wnt9a protein	BC066165	1	0	1	0	0	1.75	3.26	0.54	-2.25
<i>2900046G09Rik</i>	Hypothetical protein LOC78408	NM_133778	0	0	0	0	0	24.10	39.57	0.61	-2.25
<i>Kcnab3</i>	Voltage-gated potassium channel beta-3 subunit (K(+) channel beta-3 subunit) (Kv-beta-3)	NM_010599	0	0	0	0	0	4.85	7.87	0.62	-2.25
<i>Atrnl1</i>	Attractin-like 1	NM_181415	37	0	37	0	0	11.96	17.88	0.67	-2.24
<i>Kcnmb4</i>	Calcium activated potassium channel beta 4	NM_021452	4	0	4	0	0	8.43	12.95	0.65	-2.23
<i>Nr4a1</i>	Nuclear receptor subfamily 4, group A, member 1	NM_010444	0	0	0	0	0	26.01	42.41	0.61	-2.23
<i>Phospho1</i>	Phosphatase, orphan 1	NM_153104	0	0	0	0	0	1.90	3.41	0.56	-2.22
<i>Bai3</i>	Brain-specific angiogenesis inhibitor 3	BC032251	91	0	91	0	0	13.83	20.65	0.67	-2.21
<i>Reps2</i>	RalBP1 associated Eps domain containing protein	AK147418	4	0	4	0	0	25.57	41.37	0.62	-2.21
<i>Mamdc1</i>	Hypothetical Phenylalanine-rich region profile containing protein	AK163637	74	1	73	0	0	5.78	8.96	0.65	-2.21
<i>Emx1</i>	Empty spiracles homolog 1	NM_010131	0	0	0	0	0	0.99	1.89	0.53	-2.20
<i>Slii2</i>	Slit homolog 2 protein precursor (Slit-2)	AK220505	10	0	10	0	0	2.05	3.63	0.56	-2.20
<i>Rgs7</i>	Regulator of G protein signaling 7	NM_011880	55	1	54	0	0	9.76	15.02	0.65	-2.20
<i>Rims4</i>	Regulating synaptic membrane exocytosis 4	NM_183023	5	0	5	0	0	3.62	5.80	0.62	-2.20
<i>Osbpl10</i>	Oxysterol-binding protein-like protein 10	NM_148958	27	0	27	0	0	3.10	5.03	0.62	-2.20
<i>Slc5a7</i>	Solute carrier family 5 (choline transporter)	NM_022025	0	0	0	0	0	3.50	5.60	0.62	-2.20
<i>Tbr1</i>	T-box brain gene 1	AK158835	2	0	0	0	2	15.44	23.26	0.66	-2.19
<i>Rfx3</i>	Regulatory factor X, 3	NM_011265	30	0	30	0	0	3.30	5.27	0.63	-2.19
<i>Lynx1</i>	Ly6/neurotoxin 1	NM_011838	0	0	0	0	0	62.35	101.97	0.61	-2.19
<i>Itpka</i>	Inositol 1,4,5-trisphosphate 3-kinase A	NM_146125	0	0	0	0	0	17.25	26.73	0.65	-2.19
<i>Irx1l</i>	Hypothetical protein LOC210719	NM_177595	5	0	5	0	0	1.79	3.27	0.55	-2.19
<i>Sema5b</i>	Semaphorin-5B precursor (Semaphorin G)	BC052397	1	0	1	0	0	3.97	6.42	0.62	-2.18
<i>Hnt</i>	Neurotrimin precursor	BC023307	127	0	127	0	0	21.16	33.56	0.63	-2.18
<i>Prkag1</i>	AMP-activated protein kinase subunit gamma 1	AK157795	0	0	0	0	0	2.04	3.59	0.57	-2.18
<i>Chrm3</i>	Cholinergic receptor, muscarinic 3, cardiac	NM_033269	42	17	42	0	0	18.85	29.40	0.64	-2.17
<i>3110035E14Rik</i>	Hypothetical protein LOC76982	NM_178399	6	0	5	0	1	40.66	66.20	0.61	-2.17
<i>2610044015Rik</i>	Hypothetical protein	AK137318	1	0	1	0	0	9.02	13.90	0.65	-2.16
<i>Rit2</i>	Ras-like without CAAX 2	NM_009065	10	0	10	0	0	12.49	18.40	0.68	-2.16
<i>AK142702</i>	Hypothetical protein	AK142702	0	0	0	0	0	0.84	1.54	0.55	-2.16
<i>Egr4</i>	Early growth response 4	NM_020596	0	0	0	0	0	6.65	9.92	0.67	-2.15
<i>Mical2</i>	Flavoprotein oxidoreductase MICAL2	NM_177282	14	0	14	0	0	20.36	31.81	0.64	-2.15
<i>Sstr3</i>	Somatostatin receptor 3	NM_009218	0	0	0	0	0	2.43	4.08	0.60	-2.15
<i>Ldlr</i>	Low density lipoprotein receptor	AK170264	1	0	1	0	0	3.78	6.03	0.63	-2.14
<i>Hcn1</i>	Hyperpolarization-activated cyclic	NM_010408	23	0	23	0	0	4.69	7.45	0.63	-2.13
<i>E330039K12Rik</i>	Hypothetical homeodomain-like structure containing protein	AK220342	19	0	19	0	0	10.34	15.48	0.67	-2.13
<i>Lrrn6c</i>	Leucine rich repeat neuronal 6C	NM_175516	1	0	1	0	0	2.24	3.84	0.58	-2.13
<i>BC107398</i>	Hypothetical protein	BC107398	1	0	1	0	0	1.04	1.93	0.54	-2.13
<i>Sidt1</i>	SID1 transmembrane family, member 1	NM_198034	13	0	13	0	0	3.38	5.31	0.64	-2.12
<i>Oprd1</i>	Opioid receptor, delta 1	NM_013622	0	0	0	0	0	7.33	10.66	0.69	-2.12
<i>Insig1</i>	Insulin induced gene 1	NM_153526	0	0	0	0	0	9.29	14.22	0.65	-2.12
<i>Mib1</i>	Ubiquitin ligase mind bomb	NM_144860	15	0	12	2	1	14.45	21.16	0.68	-2.12
<i>B230343H07Rik</i>	RIKEN cDNA B230343H07	NM_001037906	19	0	19	0	0	3.48	5.48	0.64	-2.11
<i>Fxyd7</i>	FXYD domain-containing ion transport regulator	NM_022007	1	0	1	0	0	4.44	7.04	0.63	-2.11
<i>Unc5d</i>	Netrin receptor Unc5h4	NM_153135	45	0	45	0	0	1.48	2.62	0.57	-2.11
<i>Me3</i>	Hypothetical protein FLJ34862 (Malic enzyme) homolog	AK133593	2	0	2	0	0	5.74	8.73	0.66	-2.10
<i>Cacna1a</i>	Calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	AK052625	35	0	35	0	0	20.73	32.14	0.65	-2.10
<i>S69381</i>	Potassium voltage-gated channel subfamily C member 3	S69381	0	0	0	0	0	19.96	30.98	0.64	-2.10

Negr1	Neurotractin isoform a	NM_001039094	92	0	91	1	0	28.02	44.28	0.63	-2.09
AK144913	Similar to CUB and sushi multiple domains protein 2	AK144913	2	0	2	0	0	2.04	3.48	0.59	-2.09
St6galnac3	ST6	NM_011372	60	0	60	0	0	1.31	2.32	0.56	-2.09
Serpinb8	Serine protease inhibitor 8	AK048230	2	0	2	0	0	1.45	2.56	0.57	-2.09
Rnf152	RING finger protein 152	AK035832	10	0	10	0	0	0.64	1.11	0.58	-2.08
A1894139	Weakly similar to zinc finger protein ZNF65	AK133549	1	0	1	0	0	3.61	5.65	0.64	-2.08
Unc13a	Weakly similar to Munc- 13	BC058348	15	2	13	0	1	40.18	64.15	0.63	-2.08
Dlgap1	Disks large-associated protein 1 (DAP-1)	AK163689	83	1	82	0	0	25.05	39.32	0.64	-2.06
Klf16	Krueppel-like factor 16	NM_078477	0	0	0	0	0	14.71	21.28	0.69	-2.06
Slc8a1	Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein 1)	NM_011406	36	0	36	0	0	8.61	12.73	0.68	-2.06
Egr2	Early growth response 2	NM_010118	0	0	0	0	0	3.64	5.59	0.65	-2.06
Dhcr24	24-dehydrocholesterol reductase	NM_053272	0	0	0	0	0	6.85	10.00	0.69	-2.06
Galnt13	UDP-N-acetyl-alpha-D-galactosamine:polypeptide	NM_173030	26	0	26	0	0	9.46	14.28	0.66	-2.06
AK046456	Mesenchymal stem cell protein DSC54 homolog	AK046456	20	0	20	0	0	1.63	2.86	0.57	-2.05
Dock4	Dedicator of cytokinesis 4	NM_172803	47	0	46	0	1	14.46	20.85	0.69	-2.05
BC025575	Hypothetical protein LOC217219	NM_199200	0	0	0	0	0	17.20	25.89	0.66	-2.05
Ncald	Neurocalcin delta	NM_134094	34	0	34	0	0	35.45	55.75	0.64	-2.03
Nef3	Neurofilament triplet M protein (160 kDa neurofilament protein)	AK051696	0	0	0	0	0	43.91	69.36	0.63	-2.03
Neurod6	Neurogenic differentiation 6	NM_009717	0	0	0	0	0	9.52	14.29	0.67	-2.02
Sema7a	Semaphorin 7A	NM_011352	1	0	1	0	0	26.85	41.81	0.64	-2.02
Syt16	Synaptotagmin 14-like	AK137129	17	0	17	0	0	10.45	15.29	0.68	-2.02
Rims3	Hypothetical protein	AK122226	7	0	7	0	0	22.53	34.57	0.65	-2.02
AK028238	Sodium channel, voltage-gated, type I, beta polypeptide	AK028238	3	0	3	0	0	35.01	55.05	0.64	-2.02
Arf14	ADP-ribosylation factor 4-like	NM_025404	0	0	0	0	0	14.88	21.39	0.70	-2.02
AK034089	Hypothetical P-loop containing nucleotide triphosphatases structure containing protein	AK034089	6	0	6	0	0	1.05	1.86	0.57	-2.02
Cckbr	Gastrin/cholecystokinin type B receptor	BC103530	0	0	0	0	0	7.29	10.40	0.70	-2.02
Itp1r1	Inositol 1,4,5-triphosphate receptor 1	AK049015	31	1	28	0	2	69.56	109.54	0.63	-2.01
BC089626	Protein C6orf142 homolog	BC089626	9	0	8	1	0	3.45	5.26	0.66	-2.01
Eda	Ectodysplasin A (EDA protein homolog)	AJ243657	1	0	1	0	0	0.71	1.20	0.59	-2.01
Prkg1	Protein kinase, cGMP-dependent, type I alpha	NM_001013833	46	0	46	0	0	0.77	1.31	0.59	-2.01
Lsm11	U7 snRNA-associated Sm-like protein Lsm11	NM_028185	0	0	0	0	0	0.99	1.72	0.57	-2.01
Hmgcr	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	NM_008255	2	0	1	1	0	13.27	18.85	0.70	-2.01
A230078i05Rik	Hypothetical protein LOC319998	NM_177056	0	0	0	0	0	7.82	11.29	0.69	-2.00
5730507A09Rik	Hypothetical protein LOC70638	NM_183087	2	0	2	0	0	4.64	7.12	0.65	-2.00
Kcnc2	Potassium voltage gated channel, Shaw-related	NM_001025581	27	0	26	1	0	8.75	12.79	0.68	-2.00

Supplementary Table 3 ncRNAs with changes in expression levels upon TDP-43 depletion in adult mouse brain

RNAdb index	name	Chr	Start	Stop	strand	RNA-seq			Change
						RPKM in TDP-43 KD	RPKM in control	RPKM in saline	
LIT3360	reverse delta5-desaturase RNA (Revdelta5ase)	chr19	10249682	10250370	-	3.00	0.12	0.12	up
LIT1822	Kruppel-type zinc-finger protein ZIM3-like mRNA, complete sequence	chr7	6559771	6580748	-	0.62	0.01	0.01	up
LIT1602	Tsix gene	chrX	99634235	99687675	+	4.45	0.08	0.11	up
LIT1604	domesticus antisense RNA from the Xist locus, complete sequence	chrX	99634235	99687675	+	4.45	0.08	0.11	up
LIT3442	C030002C11Rik gene	chr1	196724832	196738628	+	2.96	8.63	6.81	down
LIT3440	D630033A02Rik gene	chr10	122388136	122388891	-	0.64	1.72	1.95	down
LIT3441	2210403K04Rik gene	chr11	75277842	75282884	+	1.29	3.58	3.11	down
LIT1799	clone MBI-109 miscellaneous RNA, partial sequence	chr12	90196061	90196315	+	0.19	2.00	1.95	down
LIT1623	Rian mRNA, imprinted gene	chr12	110093968	110100034	+	6.43	20.01	17.72	down
LIT1749	Mirg mRNA	chr12	110182787	110197261	+	2.12	7.39	6.70	down
LIT3409	Otx2 opposite strand (Otx2OS) RNA, variant isoform	chr14	47591238	47715298	+	0.01	0.02	0.01	down
LIT3410	Otx2 opposite strand (Otx2OS) RNA, variant isoform	chr14	47592109	47641765	+	0.01	0.02	0.01	down
LIT3411	Otx2 opposite strand (Otx2OS) RNA, variant isoform	chr14	47595527	47783406	+	0.01	0.02	0.01	down
LIT3368	RIKEN cDNA 2810037O22 gene	chr14	59340093	59342302	+	4.89	15.56	18.00	down
LIT3422	Dleu2 mRNA, partial sequence, alternatively spliced	chr14	60557141	60636460	-	0.39	0.88	1.02	down
LIT3369	retinal noncoding RNA 3 (RNCR3)	chr14	63542224	63547029	+	11.49	42.49	35.15	down
LIT3366	RIKEN cDNA 3010002C02 gene	chr16	8766673	8767567	+	6.62	13.75	18.15	down
LIT3371	retinal noncoding RNA 1 (RNCR1)	chr17	85515685	85526691	-	0.61	1.41	2.15	down
LIT2029	vault RNA, complete sequence	chr18	36927839	36927979	+	2.96	8.92	3.67	down
LIT2028	vault-associated RNA sequence	chr18	36927840	36927980	+	2.96	8.92	3.67	down
LIT3352	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA), mRNA (cDNA clone IMAGE:3582796)	chr19	5537030	5801973	-	3.61	13.25	10.70	down
LIT3351	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA), mRNA (cDNA clone IMAGE:3601939)	chr19	5625873	5801971	-	5.29	19.76	15.91	down
LIT3362	Hepcarcin RNA, complete sequence	chr19	5795689	5802671	-	123.89	522.39	428.33	down
LIT1787	clone MBI-32 miscellaneous RNA, partial sequence	chr19	5796492	5796672	-	97.17	415.23	430.62	down
LIT1651	clone MBII-386 miscellaneous RNA, partial sequence	chr19	5801468	5801548	-	53.60	219.41	222.85	down
LIT1387	U22 snoRNA host gene (UHG) gene, complete sequence	chr19	8791184	8793485	+	2.73	7.76	7.07	down
LIT1111	empty spiracles 2 opposite strand (EMX2OS)	chr19	59478353	59511885	-	0.08	0.21	0.21	down
LIT1671	Nespas mRNA	chr2	173909368	173909996	-	0.46	1.10	1.68	down
LIT3367	RIKEN cDNA 2610100L16 gene	chr3	17982103	17991742	+	2.07	4.94	7.09	down
LIT3323	RNA component of mitochondrial RNAase P (Rmrp) on chromosome 4.	chr4	43513885	43514159	-	11.64	40.17	29.24	down
LIT1806	clone MBII-109 miscellaneous RNA, partial sequence	chr4	108974503	108974582	-	15.05	38.10	3.63	down
LIT1647	clone MBII-367 miscellaneous RNA, partial sequence	chr4	131581604	131581673	+	2.12	8.30	8.88	down

LIT1313	RNA transcript from U17 small nucleolar RNA host gene	chr4	131624009	131625709	-	1.42	3.89	3.02	down
LIT1314	U17HG gene	chr4	131624010	131625709	-	1.42	3.89	3.02	down
LIT1808	clone MBII-123 miscellaneous RNA, partial sequence	chr4	148151418	148151511	-	17.86	42.33	13.45	down
LIT1345	makorin 1 pseudogene mRNA, partial sequence	chr5	89913208	89913907	-	0.48	1.69	1.18	down
LIT3370	retinal noncoding RNA 2 (RNCR2)	chr5	112453533	112456585	-	9.34	37.31	18.35	down
LIT3450	Evf1 RNA, full length	chr6	6771701	6811661	-	0.35	1.27	1.82	down
LIT1225	Mit1/Lb9 mRNA, partial sequence	chr6	30736982	30738860	+	12.42	34.37	39.93	down
LIT1226	molossinus Mit1/Lb9 gene, partial sequence	chr6	30738334	30738754	+	13.80	39.68	46.32	down
LIT2020	Y3 scRNA gene, partial sequence.	chr6	47711224	47711289	+	741.35	2636.11	1178.13	down
LIT2015	Y1 scRNA gene, partial sequence	chr6	47717676	47717749	-	703.99	2681.21	1067.28	down
LIT3416	ROSA 26 transcription 1 mRNA sequence	chr6	113036182	113042974	-	1.12	2.43	2.52	down
LIT3432	UBE3A-ATS transcript containing exon L	chr7	59091716	59094070	-	1.32	4.60	3.67	down
	lpw gene	chr7	59483753	59544353	-	0.03	0.10	0.08	down
LIT1675	lpw mRNA, partial sequence	chr7	59487027	59544354	-	0.39	1.50	1.23	down
LIT1355	Pwcr1 mRNA, complete sequence	chr7	59739300	59744327	-	0.07	0.26	0.12	down
LIT1629	KvLQT1-AS allele (LIT1)	chr7	143103111	143107841	-	0.23	0.70	0.62	down
LIT1703	7SK class III RNA gene	chr9	77960986	77961317	-	37.46	124.99	80.77	down
LIT3324	inactive X specific transcripts (Xist) on chromosome X, transcript variant 1	chrX	99663092	99685952	-	12.17	37.86	38.29	down
LIT3329	inactive X specific transcripts (Xist) on chromosome X, transcript variant 2	chrX	99663092	99685952	-	12.17	37.86	38.29	down
LIT1010	Jpx mRNA, partial sequence	chrX	99696298	99696574	+	1.64	5.92	4.94	down
LIT1761	Jpx mRNA, partial sequence	chrX	99696350	99705674	+	0.42	1.04	0.28	down
LIT1009	Jpx mRNA, partial sequence	chrX	99696350	99699246	+	0.33	0.98	3.13	down
LIT1760	Jpx mRNA, partial sequence	chrX	99696383	99705680	+	0.39	0.94	0.90	down
LIT1008	Jpx mRNA, partial sequence	chrX	99696384	99705680	+	0.39	0.94	0.90	down
LIT1006	Ftx noncoding RNA, exons 6-7	chrX	99809719	99817912	-	0.19	0.42	0.63	down
LIT1003	Ftx noncoding RNA, exons 6-7	chrX	99810272	99826413	-	0.19	0.38	0.50	down
LIT1001	Ftx noncoding RNA, exons 6-7	chrX	99810325	99812065	-	0.17	0.47	4.06	down

Supplementary Table 4 Enriched Gene Ontology terms in TDP-43 target RNAs that are downregulated upon TDP-43 depletion in adult brain

Gene Ontology Category	Enriched Gene Ontology Term		Number of listed genes in term	Total number of genes in term	% of listed genes in term	Corrected p-value*
Molecular Function	GO:0005216	ion channel activity	21	164	12.8	6.64E-12
	GO:0022838	substrate specific channel activity	21	165	12.7	3.74E-12
	GO:0015267	channel activity	21	169	12.4	3.97E-12
	GO:0022803	passive transmembrane transporter activity	21	169	12.4	3.97E-12
	GO:0005261	cation channel activity	18	115	15.7	7.19E-12
	GO:0022836	gated channel activity	19	138	13.8	9.42E-12
	GO:0046873	metal ion transmembrane transporter activity	19	146	13.0	2.13E-11
	GO:0005509	calcium ion binding	26	391	6.6	1.03E-09
	GO:0022843	voltage-gated cation channel activity	11	67	16.4	5.31E-07
	GO:0005244	voltage-gated ion channel activity	12	94	12.8	1.20E-06
	GO:0022832	voltage-gated channel activity	12	94	12.8	1.20E-06
	GO:0005262	calcium channel activity	8	34	23.5	6.74E-06
	GO:0022834	ligand-gated channel activity	8	46	17.4	5.34E-05
	GO:0015276	ligand-gated ion channel activity	8	46	17.4	5.34E-05
	GO:0031420	alkali metal ion binding	10	103	9.7	1.94E-04
	GO:0030955	potassium ion binding	8	63	12.7	3.87E-04
	GO:0005267	potassium channel activity	8	65	12.3	4.42E-04
	GO:0005249	voltage-gated potassium channel activity	7	52	13.5	1.09E-03
	GO:0005246	calcium channel regulator activity	4	8	50.0	2.00E-03
	GO:0005245	voltage-gated calcium channel activity	4	12	33.3	7.09E-03
	GO:0016247	channel regulator activity	4	13	30.8	8.62E-03
	GO:0043167	ion binding	46	2204	2.1	8.83E-03
	GO:0046872	metal ion binding	45	2157	2.1	1.06E-02
	GO:0043169	cation binding	45	2177	2.1	1.25E-02
	GO:0008066	glutamate receptor activity	4	17	23.5	1.61E-02
Cellular Component	GO:0005886	plasma membrane	61	1375	4.4	1.32E-11
	GO:0031224	intrinsic to membrane	77	2367	3.3	2.20E-09
	GO:0045202	synapse	21	220	9.5	5.97E-08
	GO:0044456	synapse part	15	143	10.5	7.11E-06
	GO:0016021	integral to membrane	67	2262	3.0	1.10E-05
	GO:0031225	anchored to membrane	12	106	11.3	6.04E-05
	GO:0044459	plasma membrane part	33	831	4.0	2.46E-04
	GO:0030054	cell junction	17	272	6.3	4.13E-04
	GO:0042734	presynaptic membrane	6	21	28.6	4.61E-04
	GO:0045211	postsynaptic membrane	9	70	12.9	4.62E-04
	GO:0034703	cation channel complex	7	48	14.6	2.64E-03
	GO:0005887	integral to plasma membrane	13	205	6.3	3.37E-03
	GO:0043005	neuron projection	12	182	6.6	4.33E-03
	GO:0034702	ion channel complex	8	76	10.5	4.16E-03
	GO:0031226	intrinsic to plasma membrane	13	214	6.1	4.01E-03
	GO:0014069	postsynaptic density	5	37	13.5	3.85E-02
Biological Process	GO:0006811	ion transport	24	360	6.7	1.23E-06
	GO:0007268	synaptic transmission	15	124	12.1	1.12E-06
	GO:0030001	metal ion transport	19	228	8.3	1.19E-06
	GO:0019226	transmission of nerve impulse	16	157	10.2	1.50E-06
	GO:0007267	cell-cell signalling	16	165	9.7	2.38E-06
	GO:0050877	neurological system process	20	284	7.0	3.25E-06
	GO:0006812	cation transport	19	275	6.9	9.59E-06
	GO:0044057	regulation of system process	13	118	11.0	1.34E-05
	GO:0006816	calcium ion transport	10	72	13.9	8.28E-05
	GO:0015674	di-, tri-valent inorganic cation transport	10	92	10.9	5.95E-04
	GO:0050804	regulation of synaptic transmission	9	70	12.9	5.56E-04
	GO:0046903	secretion	11	118	9.3	5.54E-04
	GO:0048878	chemical homeostasis	14	205	6.8	5.46E-04
	GO:0051969	regulation of transmission of nerve impulse	9	73	12.3	6.00E-04
	GO:0006873	cellular ion homeostasis	12	152	7.9	7.05E-04
	GO:0031644	regulation of neurological system process	9	76	11.8	7.09E-04
	GO:0055082	cellular chemical homeostasis	12	156	7.7	7.96E-04
	GO:0032940	secretion by cell	10	103	9.7	8.34E-04
	GO:0006813	potassium ion transport	9	85	10.6	1.37E-03
	GO:0050801	ion homeostasis	12	168	7.1	1.35E-03
	GO:0006887	exocytosis	8	66	12.1	1.81E-03
	GO:0019725	cellular homeostasis	13	209	6.2	1.96E-03
	GO:0030182	neuron differentiation	13	221	5.9	3.21E-03
	GO:0015672	monovalent inorganic cation transport	11	158	7.0	3.47E-03
	GO:0006836	neurotransmitter transport	7	52	13.5	3.34E-03
	GO:0042391	regulation of membrane potential	8	79	10.1	4.63E-03
	GO:0007610	behavior	12	200	6.0	4.86E-03
	GO:0048666	neuron development	11	170	6.5	5.44E-03
	GO:0031175	neuron projection development	10	141	7.1	6.04E-03
	GO:0007186	G-protein coupled receptor protein signalling pathway	12	207	5.8	5.91E-03

GO:0042592	homeostatic process	15	329	4.6	8.13E-03
GO:0051899	membrane depolarization	5	26	19.2	1.27E-02
GO:0003001	generation of a signal involved in cell-cell signaling	6	48	12.5	1.56E-02
GO:0006874	cellular calcium ion homeostasis	6	52	11.5	2.19E-02
GO:0055074	calcium ion homeostasis	6	54	11.1	2.53E-02
GO:0055066	di-, tri-valent inorganic cation homeostasis	7	82	8.5	2.75E-02
GO:0050905	neuromuscular process	5	33	15.2	2.76E-02
GO:0007626	locomotory behavior	8	113	7.1	2.77E-02
GO:0048812	neuron projection morphogenesis	8	114	7.0	2.84E-02
GO:0006875	cellular metal ion homeostasis	6	57	10.5	2.82E-02
GO:0048667	cell morphogenesis involved in neuron differentiation	8	115	7.0	2.84E-02
GO:0055065	metal ion homeostasis	6	59	10.2	3.14E-02
GO:0007611	learning or memory	6	60	10.0	3.30E-02
GO:0007612	learning	5	38	13.2	3.94E-02
GO:0007628	adult walking behavior	4	19	21.1	4.33E-02

*The p-value indicated is corrected for multiple testing using the Benjamini-Hochberg method.

Supplementary Table 5 TDP-43 binding and regulation on transcripts encoding for proteins involved in RNA metabolism

Gene symbol	Protein	Refseq/mRNA identifier	Number of CLIP-seq clusters					RNA-seq			Splicing changes	
			Total	in 5'UTR	in introns	in exons	in 3'UTR	RPKM in TDP-43 KD	RPKM in control	Ratio KD/control	Z score	Change upon TDP-43 depletion (exon coordinates)
<i>A2bp1/Fox1</i>	Ataxin-2 binding protein 1	AY659958	309	1	308	0	0	52.07	53.16	0.98	-0.02	More exclusion (chr16:7307308-7307361)
<i>Adar1 (ADAR2)</i>	Adenosine deaminase, RNA-specific, B1	NM_001024839	14	0	14	0	0	21.21	27.16	0.78	-1.24	No
<i>Als4</i>	Serataxin	NM_198033	1	0	1	0	0	13.72	12.97	1.06	0.04	No
<i>Atxn2</i>	Ataxin-2	NM_009125	18	0	18	0	0	18.71	15.96	1.17	0.58	No
<i>Cugbp1</i>	CUG triplet repeat, RNA-binding protein 1	NM_017368	17	0	17	0	0	34.87	37.92	0.92	-0.35	No
<i>Elavl1</i>	ELAV	NM_010485	2	0	2	0	0	17.20	16.79	1.02	-0.09	No
<i>Elavl2</i>	ELAV-like protein 2 (Hu-antigen B)	BC049125	17	0	17	0	0	9.71	11.13	0.87	-0.91	No
<i>Elavl3</i>	ELAV-like protein 3	NM_010487	7	0	7	0	0	35.32	35.20	1.00	0.05	No
<i>Elavl4</i>	ELAV-like 4 isoform a	NM_010488	8	0	8	0	0	14.14	14.16	1.00	-0.23	No
<i>Elp3</i>	Elongation protein 3 homolog	AK088457	3	0	3	0	0	15.61	17.54	0.89	-0.81	No
<i>Ewsr1</i>	Ewing sarcoma homolog	AK147909	8	0	6	0	2	44.86	48.66	0.92	-0.31	No
<i>Fus</i>	Fus/TLS protein	BC011078	4	0	0	3	1	92.88	129.56	0.72	-1.46	No
<i>Fusip1</i>	FUS interacting protein	AK169071	3	0	1	0	2	16.64	17.47	0.95	-0.46	No
<i>Mbnl1</i>	Muscleblind-like 1	NM_020007	19	0	19	0	0	39.54	34.50	1.15	0.69	No
<i>Mbnl2</i>	Muscleblind-like 2	AK164372	14	0	14	0	0	68.83	66.40	1.04	0.24	No
<i>Nova1</i>	Neuro-oncological ventral antigen 1	NM_021361.1	15	0	13	0	2	7.62	16.97	0.45		No
<i>Nova2</i>	Neuro-oncological ventral antigen 2	NM_001029877.	7	0	6	0	1	15.04	36.85	0.41		No
<i>Ptbp2</i>	Polypyrimidine tract binding protein 2	NM_019550	3	0	3	0	0	21.64	21.98	0.98	-0.17	More exclusion (chr3:119716615-119716649)
<i>Raly</i>	hnRNP-associated with lethal yellow	NM_023130	9	0	9	0	0	17.42	19.52	0.89	-0.73	More exclusion (chr2:154551351-154551399)
<i>Rbm9/Fox2</i>	Fox-1 homolog	AK044929	32	0	32	0	0	45.73	54.32	0.84	-0.72	No
<i>Sfrs9</i>	Splicing factor, arginine/serine rich 9	NM_025573	1	0	1	0	0	13.12	12.28	1.07	0.08	No
<i>Taf15</i>	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68 kDa	AK011843	5	0	5	0	0	26.82	28.03	0.96	-0.22	No
<i>Tia1</i>	Cytotoxic granule-associated RNA binding protein	NM_011585	6	0	6	0	0	26.46	21.48	1.23	0.92	More inclusion (chr6:86384734-86384767)

Coordinates on mm8 mouse genome. *Human orthologue gene.

Supplementary Table 6 TDP-43 binding and regulation on transcripts associated with disease

Gene symbol	Protein	Refseq/mRNA identifier	Number of CLIP-seq clusters					RNA-seq			Splicing changes	
			Total	in 5'UTR	in introns	in exons	in 3'UTR	RPKM in TDP-43 KD	RPKM in control	Ratio KD/control	Z score	Change upon TDP-43 depletion (exon coordinates)
<i>Adarb1</i> (ADAR2)*	Adenosine deaminase, RNA-specific, B1	NM_001024839	14	0	14	0	0	21.21	27.16	0.78	-1.24	No
<i>Als2</i>	Alsin	AK020484	8	0	8	0	0	6.67	6.94	0.96	-0.55	No
<i>Als4</i>	Senataxin	NM_198033	1	0	1	0	0	13.72	12.97	1.06	0.04	No
<i>Ang1</i>	Angiogenin	NM_007447	0	0	0	0	0	21.94	9.78	2.24	3.79	No
<i>App</i>	Amyloid beta precursor protein	AK148439	34	0	29	3	2	219.61	263.72	0.83	-0.77	No
<i>Ar</i>	Androgen receptor	NM_013476	0	0	0	0	0	2.90	2.73	1.06	-0.33	No
<i>Atxn1</i>	Ataxin-1	NM_009124	64	0	64	0	0	16.02	19.97	0.80	-1.31	No
<i>Atxn10</i>	Ataxin-10	NM_016843	9	0	9	0	0	43.25	40.78	1.06	0.30	No
<i>Atxn2</i>	Ataxin-2	NM_009125	18	0	18	0	0	18.71	15.96	1.17	0.58	No
<i>Atxn7</i>	Ataxin-7	NM_139227	4	0	3	0	1	6.55	6.70	0.98	-0.45	No
<i>Cacna1c</i>	Calcium channel, voltage-dependent, L type	NM_009781	77	0	77	0	0	5.57	9.56	0.58	-2.65	No
<i>Chmp2b</i>	Chromatin modifying protein 2B	NM_026879	1	0	1	0	0	16.51	12.82	1.29	0.96	No
<i>Dctn1</i>	Dynactin 1	AK157867	8	0	8	0	0	40.37	50.11	0.81	-0.93	No
<i>Eip3</i>	Elongation protein 3 homolog	AK088457	3	0	3	0	0	15.61	17.54	0.89	-0.81	No
<i>Fbxo7</i>	F-box only protein 7	BC032153	5	0	5	0	0	9.99	7.35	1.36	0.95	No
<i>Fgf14</i>	Fibroblast growth factor 14 isoform b	NM_207667	85	0	85	0	0	6.99	14.99	0.47	-3.76	No
<i>Fig4</i>	Sac domain-containing inositol phosphatase 3	NM_133999	3	0	3	0	0	10.36	8.58	1.21	0.50	No
<i>Fmr1</i>	Fragile X mental retardation protein 1	NM_008031	0	0	0	0	0	17.03	17.38	0.98	-0.31	No
<i>Fus/Tls</i>	Fus/Tls protein	BC011078	4	0	0	3	1	92.88	129.56	0.72	-1.46	No
<i>Fxn</i>	Frataxin	BC058533	0	0	0	0	0	1.57	1.10	1.43	0.41	No
<i>Gria2</i>	Glutamate receptor, ionotropic, AMPA2 (alpha 2)	NM_001039195	18	1	14	0	3	105.96	110.65	0.96	-0.12	No
<i>Gria3</i>	Glutamate receptor, ionotropic, AMPA3 (alpha)	NM_016886	18	0	17	0	1	33.82	45.41	0.74	-1.35	More exclusion (chrX:37898880-37914127)
<i>Grik2</i>	Glutamate receptor, ionotropic, kainate 2 (beta)	NM_010349	52	0	52	0	0	17.00	27.85	0.61	-2.46	No
<i>Grin1</i>	Glutamate receptor, ionotropic, NMDA1 (zeta 1)	BC039157	3	0	3	0	0	62.95	83.99	0.75	-1.25	More exclusion (chr2:25133351-25133414)
<i>Grin2a</i>	Glutamate receptor, ionotropic, NMDA2A (epsilon)	NM_008170	83	0	83	0	0	2.19	4.23	0.52	-2.56	No
<i>Grin2c</i>	Glutamate receptor, ionotropic, NMDA2C (epsilon)	NM_010350	3	0	3	0	0	7.38	11.76	0.63	-2.45	No
<i>Grn</i>	Progranulin	NM_008175	1	0	0	0	1	70.17	23.12	3.04	5.22	no
<i>Hdac6</i>	Histone deacetylase 6	NM_010413	3	0	3	0	0	8.98	10.54	0.85	-1.05	No
<i>Hdh</i>	Huntingtin	NM_010414	10	0	9	1	0	8.52	16.55	0.51	-3.29	No
<i>Ighmbp2</i>	Immunoglobulin mu binding protein 2	NM_009212	1	0	1	0	0	3.26	2.98	1.09	-0.19	No
<i>Kcnma1</i>	Calcium-activated potassium channel alpha subunit 1 (Calcium-activated potassium channel, subfamily M, alpha subunit 1)	U09383	96	0	96	0	0	8.34	14.36	0.58	-2.66	No
<i>Kif5a</i>	Kinesin family member 5A	NM_001039000	5	0	2	0	3	261.61	364.81	0.72	-1.45	No
<i>Kifap3</i>	Kinesin-associated protein 3	NM_010629	5	0	5	0	0	43.38	50.66	0.86	-0.65	No

<i>Lrrk2</i>	Leucine-rich repeat kinase 2	NM_025730	4	0	4	0	0	11.28	14.49	0.78	-1.41	No
<i>Mapt</i>	Tau protein	NM_001038609	10	0	10	0	0	80.18	97.03	0.83	-0.80	No
<i>Mecp2</i>	Methyl CpG binding protein 2	AK158664	4	0	4	0	0	29.52	30.32	0.97	-0.15	No
<i>Mjd/Atxn3</i>	Mjd/Ataxin-3 protein	BC087880	3	0	3	0	0	9.65	8.49	1.14	0.21	No
<i>Nefl</i>	Neurofilament, light polypeptide	NM_010910	1	0	0	0	1	40.04	61.29	0.65	-1.88	No
<i>Nlgn1</i>	Neuroligin 1	NM_138666	102	0	101	1	0	8.55	16.28	0.53	-3.19	No
<i>Nrxn1</i>	Neurexin-I-alpha precursor (Neurexin I-alpha)	AB093249	162	0	162	0	0	18.66	33.28	0.56	-2.76	No
<i>Nrxn2</i>	Hypothetical Laminin G	AK163904	28	0	27	0	1	41.94	45.65	0.92	-0.34	More exclusion (chr19:6513715-6513805)
<i>Nrxn3</i>	Neurexin III	BC060719	178	0	178	0	0	16.25	37.23	0.44	-3.93	More inclusion (chr12:90604171-90604261)
<i>Optn</i>	Optineurin	NM_181848	1	0	1	0	0	6.07	5.06	1.20	0.29	No
<i>Park2</i>	Parkin	AF250294	39	0	39	0	0	0.63	2.18	0.29	-3.78	No
<i>Park7</i>	DJ-1 protein	NM_020569	0	0	0	0	0	15.89	14.92	1.06	0.07	No
<i>Pink1</i>	PTEN induced putative kinase 1	NM_026880	0	0	0	0	0	81.90	82.18	1.00	0.06	No
<i>Pla2g6</i>	Phospholipase A2, group VI	NM_016915	0	0	0	0	0	2.70	3.00	0.90	-0.81	No
<i>Prnp</i>	Prion protein	NM_011170	4	0	2	1	1	179.48	153.18	1.17	0.81	No
<i>Psen1</i>	Presenilin 1	NM_008943	4	1	3	0	0	18.45	16.55	1.11	0.34	No
<i>Psen2</i>	Presenilin 2	AF038935	1	0	1	0	0	4.09	3.29	1.24	0.23	No
<i>Slc1a2/Glt1 (EAAT2)*</i>	Solute carrier family 1	NM_011393	28	0	26	1	1	139.06	156.13	0.89	-0.46	No
<i>Slc1a3 (EAAT1)*</i>	Solute carrier family 1	NM_148938	2	0	2	0	0	134.38	97.73	1.37	1.55	No
<i>Slc1a6 (EAAT4)*</i>	Solute carrier family 1	NM_009200	3	0	3	0	0	1.27	1.32	0.96	-0.63	No
<i>Smn1</i>	Survival motor neuron protein	BC045158	0	0	0	0	0	6.40	5.76	1.11	0.01	No
<i>Sncb</i>	Synuclein, alpha	AK014472	3	0	2	0	1	37.26	42.97	0.87	-0.63	No
<i>Sncb</i>	Synuclein, beta	NM_033610	3	1	1	0	1	54.68	68.33	0.80	-0.95	No
<i>Sod1</i>	Superoxide dismutase 1	BC057074	0	0	0	0	0	49.95	45.48	1.10	0.50	No
<i>Sort1</i>	Sortilin 1	NM_019972	8	0	8	0	0	75.67	86.65	0.87	-0.55	More inclusion (chr3:108483527-108483626)
<i>Spg11</i>	Spatacsin	BC019404	4	0	4	0	0	4.75	4.26	1.12	-0.04	No
<i>Tbp</i>	TATA binding protein	BC016476	0	0	0	0	0	7.33	6.06	1.21	0.35	No
<i>Tnrc15/Gigyf2</i>	Tnrc15 protein	BC027137	15	1	14	0	1	14.87	13.80	1.08	0.12	No
<i>Ube3a</i>	Ubiquitin protein ligase E3A isoform 1	NM_173010	3	0	3	0	0	23.19	19.27	1.20	0.80	No
<i>Uchl1</i>	Ubiquitin carboxy-terminal hydrolase L1	NM_011670	0	0	0	0	0	93.43	90.90	1.03	0.20	No
<i>Vapb</i>	Vesicle-associated membrane protein, associated	NM_019806	7	2	5	0	2	23.29	26.90	0.87	-0.73	No
<i>Vcp</i>	Valosin containing protein	NM_009503	1	0	1	0	0	11.57	9.91	1.17	0.43	No

Z-scores between -1.96 and 1.96 represent p-values greater than 0.05. Coordinates on mm8 mouse genome. *Human orthologue gene.